

REPLACEMENT SHEET

Figure 2. Sequence of C5 H6p WNV *prM-M-E* C5 in pDS-2646-1-1

⇒C5R

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1   TGAATGTTAA ATGTTATACT TTGGATGAAG CTATAAATAT GCATTGGAAA AATAATCCAT
61  TTAAAGAAAG GATTCAAATA CTACAAAACC TAAGCGATAA TATGTTAACT AAGCTTATTC
121 TTAACGACGC TTTAAATATA CACAAATAAA CATAAATTTT GTATAACCTA ACAAATAACT
181 AAAACATAAA AATAATAAAA GGAAATGTAA TATCGTAATT ATTTTACTCA GGAATGGGGT
241 TAAATATTTA TATCACGTGT ATATCTATAC TGTTATCGTA TACTCTTTAC AATTACTATT
301 ACGAATATGC AAGAGATAAT AAGATTACGT ATTTAAGAGA ATCTTGTCAT GATAATTGGG
361 TACGACATAG TGATAAATGC TATTTGCGAT CGTTACATAA AGTCAGTTGG AAAGATGGAT
421 TTGACAGATG TAACTTAATA GGTGCAAAAA TGTTAAATAA CAGCATTCTA TCGGAAGATA
481 GGATACCAGT TATATTATAC AAAAATCACT GGTGGGATAA AACAGATTCT GCAATATTTCG
541 TAAAAGATGA AGATTACTGC GAATTTGTAA ACTATGACAA TAAAAAGCCA TTTATCTCAA
601 CGACATCGTG TAATTCTTCC ATGTTTTATG TATGTGTTTC AGATATTATG AGATTACTAT
661 AAACTTTTTG TATACTTATA TTCCGTAAAC TATATTAATC ATGAAGAAAA TGAAAAAGTA
721 TAGAAGCTGT TCACGAGCGG TTGTTGAAAA CAACAAAATT ATACATTCAA GATGGCTTAC
781 ATATACGTCT GTGAGGCTAT CATGGATAAT GACAATGCAT CTCTAAATAG GTTTTTGGAC
841 AATGGATTGG ACCCTAACAC GGAATATGGT ACTCTACAAT CTCCTCTTGA AATGGCTGTA
901 ATGTTCAAGA ATACCGAGGC TATAAAAATC TTGATGAGGT ATGGAGCTAA ACCTGTAGTT
961 ACTGAATGCA CAACTTCTTG TCTGCATGAT GCGGTGTTGA GAGACGACTA CAAAATAGTG
1021 AAAGATCTGT TGAAGAATAA CTATGTAAAC AATGTTCTTT ACAGCGGAGG CTTTACTCCT
1081 TTGTGTTTGG CAGCTTACCT TAACAAAGTT AATTTGGTTA AACTTCTATT GGCTCATTCG
1141 GCGGATGTAG ATATTTCAAA CACGGATCGG TTAACCTCTC TACATATAGC CGTATCAAAT
1201 AAAAATTTAA CAATGGTTAA ACTTCTATTG AACAAAGGTG CTGATACTGA CTTGCTGGAT
1261 AACATGGGAC GTACTCCTTT AATGATCGCT GTACAATCTG GAAATATTGA AATATGTAGC
1321 ACACTACTTA AAAAAAATAA AATGTCCAGA ACTGGGAAAA ATTGATCTTG CCAGCTGTAA
1381 TTCATGGTAG AAAAGAAGTG CTCAGGCTAC TTTTCAACAA AGGAGCAGAT GTAAACTACA
1441 TCTTTGAAAG AAATGGAAAA TCATATACTG TTTTGGAAAT GATTAAAGAA AGTTACTCTG
1501 AGACACAAAA GAGGTAGCTG AAGTGGTACT CTCAAAAAGG TACGTGACTA ATTAGCTATA
1561 AAAAGGATCC GGGTTAATTA ATTAGTCATC AGGCAGGGCG AGAACGAGAC TATCTGCTCG
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REPLACEMENT SHEET

Figure 2 continued

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                                     ⇒ H6p
1621   TTAATTAATT AGAGCTTCTT TATTCTATAC TAAAAAGTG AAAATAAATA CAAAGGTTCT
1681   TGAGGGTTGT GTTAAATTGA AAGCGAGAAA TAATCATAAA TTATTCATT ATCGCGATAT

                                     ⇒ WNV capsid leader
                                     M   T   G   I   A   V   M   I   G   L   I   A   S   V   .
1741   CCGTTAAGTT TGTATCGTAA TGACCGGAAT TGCAGTCATG ATTGGCCTGA TCGCCAGCGT

                                     ⇒ WNV prM
.   G   A   V   T   L   S   N   F   Q   G   K   V   M   M   T   V   N   A   T   D   .
1801   AGGAGCAGTT ACCCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA

.   V   T   D   V   I   T   I   P   T   A   A   G   K   N   L   C   I   V   R   A   .
1861   CGTCACAGAT GTCATCACGA TTCCAACAGC TGCTGGAAAG AACCTATGCA TTGTCTAGAGC

.   M   D   V   G   Y   M   C   D   D   T   I   T   Y   E   C   P   V   L   S   A   .
1921   AATGGATGTG GGATACATGT GCGATGATAC TATCACTTAT GAATGCCCAG TGCTGTCCGC

.   G   N   D   P   E   D   I   D   C   W   C   T   K   S   A   V   Y   V   R   Y   .
1981   TGGTAATGAT CCAGAAGACA TCGACTGTTG GTGCACAAAG TCAGCAGTCT ACGTCAGGTA

                                     ⇒ WNV M
.   G   R   C   T   K   T   R   H   S   R   R   S   R   R   S   L   T   V   Q   T   .
2041   TGGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGGTCACTGA CAGTGCAGAC

.   H   G   E   S   T   L   A   N   K   K   G   A   W   M   D   S   T   K   A   T   .
2101   ACACGGAGAA AGCACTCTAG CGAACAAGAA GGGGGCTTGG ATGGACAGCA CCAAGGCCAC

.   R   Y   L   V   K   T   E   S   W   I   L   R   N   P   G   Y   A   L   V   A   .
2161   AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CCTGGATATG CCCTGGTGGC

.   A   V   I   G   W   M   L   G   S   N   T   M   Q   R   V   V   F   V   V   L   .
2221   AGCCGTCATT GGTGGATGTC TTGGGAGCAA CACCATGCAG AGAGTTGTGT TTGTGCTGCT

                                     ⇒ WNV E
.   L   L   L   V   A   P   A   Y   S   F   N   C   L   G   M   S   N   R   D   F   .
2281   ATTGCTTTTG GTGGCCCCAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT

.   L   E   G   V   S   G   A   T   W   V   D   L   V   L   E   G   D   S   C   V   .
2341   CTTGGAAGGA GTGTCTGGAG CAACATGGGT GGATTGTTT CTCGAAGGCG ACAGCTGCGT

.   T   I   M   S   K   D   K   P   T   I   D   V   K   M   M   N   M   E   A   A   .
2401   GACTATCATG TCTAAGGACA AGCCTACCAT CGATGTGAAG ATGATGAATA TGGAGGCGGC

.   N   L   A   E   V   R   S   Y   C   Y   L   A   T   V   S   D   L   S   T   K   .
2461   CAACCTGGCA GAGGTCCGCA GTTATTGCTA TTTGGCTACC GTCAGCGATC TCTCCACCAA

.   A   A   C   P   T   M   G   E   A   H   N   D   K   R   A   D   P   A   F   V   .
2521   AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGCTGACC CAGCTTTTGT

.   C   R   Q   G   V   V   D   R   G   W   G   N   G   C   G   L   F   G   K   G   .
2581   GTGCAGACAA GGAGTGGTGG ACAGGGGCTG GGGCAACGGC TGCAGACTAT TTGGCAAAGG

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REPLACEMENT SHEET

Figure 2 continued

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      . S I D   T C A K   F A C   S T K   A I G R   T I L .
2641  AAGCATTGAC ACATGCGCCA AATTTGCCTG CTCTACCAAG GCAATAGGAA GAACCATCTT
      mutated T5NT
      . K E N   I K Y E   V A I   F V H   G P T T   V E S .
2701  GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTTCGTGCAC GGACCAACTA CTGTGGAGTC

      . H G N   Y S T Q   V G A   T Q A   G R F S   I T P .
2761  GCACGGAAAC TACTCCACAC AGGTTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

      . A A P   S Y T L   K L G   E Y G   E V T V   D C E .
2821  TGCGGCGCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

      . P R S   G I D T   N A Y   Y V M   T V G T   K T F .
2881  ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTTGGAA CAAAGACGTT

      . L V H   R E W F   M D L   N L P   W S S A   G S T .
2941  CTTGGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

      . V W R   N R E T   L M E   F E E   P H A T   K Q S .
3001  TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

      . V I A   L G S Q   E G A   L H Q   A L A G   A I P .
3061  TGTGATAGCA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGCTG GAGCCATTCC

      . V E F   S S N T   V K L   T S G   H L K C   R V K .
3121  TGTGGAATTT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTTGAAGT GTAGAGTGAA

      . M E K   L Q L K   G T T   Y G V   C S K A   F K F .
3181  GATGGAAAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

      . L G T   P A D T   G H G   T V V   L E L Q   Y T G .
3241  TCTTGGGACT CCCGCAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

      . T D G   P C K V   P I S   S A A   S L N D   L T P .
3301  CACGGATGGA CCTTGCAAAG TTCCTATCTC GTCAGCGGCT TCATTGAACG ACCTAACGCC

      . V G R   L V T V   N P F   V S V   A T A N   A K V .
3361  AGTGGGCAGA TTGGTCACTG TCAACCCTTT TGTTTCAGTG GCCACGGCCA ACGCTAAGST

      . L I E   L E P P   F G D   S Y I   V V G R   G E Q .
3421  CCTGATTGAA TTGGAACCAC CCTTTGGAGA CTCATACATA GTGGTGGGCA GAGGAGAACA

      . Q I N   H H W H   K S G   S S I   G K A F   T T T .
3481  ACAGATCAAT CACCATTGGC ACAAGTCTGG AAGCAGCATT GGCAAAGCCT TTACAACCAC

      . L K G   A Q R L   A A L   G D T   A W D F   G S V .
3541  CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGGAGACACA GCTTGGGACT TTGGATCAGT

      . G G V   F T S V   G K A   V H Q   V F G G   A F R .
3601  TGGAGGGGTG TTCACCTCAG TTGGGAAGGC TGTCCATCAA GTGTTTCGGAG GAGCATTCCG

      . S L F   G G M S   W I T   Q G L   L G A L   L L W .
3661  CTCACTGTTC GGAGGCATGT CCTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTTGTG

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REPLACEMENT SHEET

Figure 2 continued

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. M G I N A R D R S I A L T F L A V G G V .  
3721 GATGGGCATC AATGCTCGTG ATAGGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT  
  
. L L F L S V N V H A  
3781 TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTTA TCTAGAATCG ATCCCGGGTT  
                                     ==> C5L  
3841 TTTATGACTA GTTAATCACG GCCGCCTTAT AAAGATCTAA AATGCATAAT TTCTAAATAA  
  
3901 TGAAAAAAG TACATCATGA GCAACGCGTT AGTATATTTT ACAATGGAGA TTAACGCTCT  
  
3961 ATACCGTTCT ATGTTTATTG ATTCAGATGA TGTTTTAGAA AAGAAAGTTA TTGAATATGA  
  
4021 AAACTTTAAT GAAGATGAAG ATGACGACGA TGATTATTGT TGTAAATCTG TTTTAGATGA  
  
4081 AGAAGATGAC GCGCTAAAGT ATACTATGGT TACAAAGTAT AAGTCTATAC TACTAATGGC  
  
4141 GACTTGTCGA AGAAGGTATA GTATAGTGAA AATGTTGTTA GATTATGATT ATGAAAAACC  
  
4201 AAATAAATCA GATCCATATC TAAAGGTATC TCCTTTGCAC ATAATTTTAT CTATTCTAG  
  
4261 TTTAGAATAC
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REPLACEMENT SHEET

Figure 4. Sequence of F8 H6p WNV prM-M-E F8 in pSL-5513-1-1-1.

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⇒ F8R
1  GACCCTTTAC AAGAATAAAA GAAGAAACAA CTGTGAAATA GTTTATAAAT GTAATTCGTA
61  TGCAGAAAAC GATAATATAT TTTGGTATGA GAAATCTAAA GGAGACATAG TTTGTATAGA
121 CATGCGCTCT TCCGATGAGA TATTOGATGC TTTTCTAATG TATCATATAG CTACAAGATA
181 TGCCTATCAT GATGATGATA TATATCTACA AATAGTGTTA TATTATTCTA ATAATCAAAA
241 TGTATATCT TATATTACGA AAAATAAATA CGTTAAGTAT ATAAGAAATA AAAC TAGAGA
301 CGATATTCAT AAAGTAAAAA TATTAGCTCT AGAAGACTTT ACAACGGAAG AAATATATTG
361 TTGGATTAGT AATATATAAC AGCGTAGCTG CACGGTTTTG ATCATTTTCC AACAAATATA
421 ACCAATGAAG GAGGACGACT CATCAAACAT AAATAACATT CACGGAAAAT ATTCAGTATC
481 AGATTTTATCA CAAGATGATT ATGTTATTGA ATGTATAGAC GGATCTTTTG ATTCGATCAA
541 GTATAGAGAT ATAAAGGTTA TAATAATGAA GAATAACGGT TACGTTAATT GTAGTAAATT
601 ATGTAAAATG CGGAATAAAT ACTTTTCTAG ATGGTTGCGT CTTTCTACTT CTAAAGCATT
661 ATTAGACATT TACAATAATA AGTCAGTAGA TAATGCTATT GTTAAAGTCT ATGGTAAAGG
721 TAAGAACTT ATTATAACAG GATTTTATCT CAAACAAAAT ATGATACGTT ATGTTATTGA
781 GTGGATAGGG GATGATTTTA CAAACGATAT ATACAAAATG ATTAATTTCT ATAATGCGTT
841 ATTCGGTAAC GATGAATTAA AAATAGTATC CTGTGAAAAC ACTCTATGCC CGTTTATAGA
901 ACTTGGTAGA TGCTATTATG GTAAAAATG TAAGTATATA CACGGAGATC AATGTGATAT
961 CTGTGGTCTA TATATACTAC ACCCTACCGA TATTAACCAA CGAGTTTCTC ACAAGAAAAC
1021 TTGTTTAGTA GATAGAGATT CTTTGATTGT GTTTAAAAGA AGTACCAGTA AAAAGTGTGG
1081 CATATGCATA GAAGAAATAA ACAAAAAACA TATTTCCGAA CAGTATTTTG GAATTCTCCC
1141 AAGTTGTAAA CATATTTTTT GCCTATCATG TATAAGACGT TGGGCGAGATA CTACCAGAAA
1201 TACAGATACT GAAAATACGT GTCCTGAATG TAGAATAGTT TTTCCTTTCA TAATACCCAG
1261 TAGGTATTGG ATAGATAATA AATATGATAA AAAAATATTA TATAATAGAT ATAAGAAAAT
1321 GATTTTITACA AAAATACCTA TAAGAACAAT AAAAATATAA TTACATTTAC GGAAAATAGC
1381 TGGTTTTAGT TTACCAACTT AGAGTAATTA TCATATTGAA TCTATATTGC TAATTAGCTA
1441 ATAAAAACCC GGGTTAATTA ATTAGTCATC AGGCAGGGCG AGAACGAGAC TATCTGCTCG

⇒ H6p
1501 TTAATTAATT AGAGCTTCTT TATTCTATAC TTAAAAAGTG AAAATAAATA CAAAGGTTCT

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REPLACEMENT SHEET

Figure 4 continued

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1561  TGAGGGTTGT GTTAAATTGA AAGCGAGAAA TAATCATAAA TTATTCATT ATCGCGATAT
                                     ⇒ WNV capsid leader
                                     M T G I A V M I G L I A S V .
1621  CCGTTAAGTT TGTATCGTAA TGACCGGAAT TSCAGTCATS ATTGGCCTGA TCGCCAGCGT
                                     ⇒ WNV prM
. G A V T L S N F Q G K V M M T V N A T D .
1681  AGGAGCGGTT ACCCTCTCTA ACTTCCAAGG GAAGGTGATG ATGACGGTAA ATGCTACTGA
. V T D V I T I P T A A G K N L C I V R A .
1741  CGTCACAGAT GTCATCACGA TTCCAACAGC TGCTGGAAAG AACCTATGCA TTGTCAGAGC
. M D V G Y M C D D T I T Y E C P V L S A .
1801  AATGGATGTG GGATACATGT GCGATGATAC TATCACTTAT GAATGCCCAG TGCTGTCCGC
. G N D P E D I D C W C T K S A V Y V R Y .
1861  TGGTAATGAT CCAGAAGACA TCGACTGTTG GTGCACAAAG TCAGCAGTCT ACGTCAGGTA
                                     ⇒ WNV M
. G R C T K T R H S R R S R R S L T V Q T .
1921  TGGAAGATGC ACCAAGACAC GCCACTCAAG ACGCAGTCGG AGGTCACTGA CAGTGCAGAC
. H G E S T L A N K K G A W M D S T K A T .
1981  ACACGGAGAA AGCACTCTAG CGAACAAGAA GGGGGCTTGG ATGGACAGCA CCAAGGCCAC
. R Y L V K T E S W I L R N P G Y A L V A .
2041  AAGGTATTTG GTAAAAACAG AATCATGGAT CTTGAGGAAC CCTGGATATG CCCTGGTGGC
. A V I G W M L G S N T M Q R V V F V V L .
2101  AGCCGTCATT GGTTGGATGC TTGGGAGCAA CACCATGCAG AGAGTTGTGT TTGTGCGTCT
                                     ⇒ WNV E
. L L L V A P A Y S F N C L G M S N R D F .
2161  ATTGCTTTTG GTGGCCCCAG CTTACAGCTT CAACTGCCTT GGAATGAGCA ACAGAGACTT
. L E G V S G A T W V D L V L E G D S C V .
2221  CTTGGAAGGA GTGTCTGGAG CAACATGGGT GGATTTGGTT CTCGAAGGCG ACAGCTGCGT
. T I M S K D K P T I D V K M M N M E A A .
2281  GACTATCATG TCTAAGGACA AGCCTACCAT CGATGTGAAG ATGATGAATA TGGAGGCGGC
. N L A E V R S Y C Y L A T V S D L S T K .
2341  CAACCTGGCA GAGGTCCGCA GTTATTGCTA TTTGGCTACC GTCAGCGATC TCTCCACCAA
. A A C P T M G E A H N D K R A D P A F V .
2401  AGCTGCGTGC CCGACCATGG GAGAAGCTCA CAATGACAAA CGTGCTGACC CAGCTTTTGT
. C R Q G V V D R G W G N G C G L F G K G .
2461  GTGCAGACAA GGAGTGGTGG ACAGGGGCTG GGGCAACGGC TGCGGACTAT TTGGCAAAGG
. S I D T C A K F A C S T K A I G R T I L .
2521  AAGCATTGAC ACATGCGCCA AATTTGCCTG CTCTACCAAG GCAATAGGAA GAACCATCTT

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REPLACEMENT SHEET

Figure 4 continued

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2581 . K E N I K Y E V A I F V H G P T T V E S .
    GAAAGAGAAT ATCAAGTACG AAGTGGCCAT CTTCTGTGCAC GGACCAACTA CTGTGGAGTC

2641 . H G N Y S T Q V G A T Q A G R F S I T P .
    GCACGGAAAC TACTCCACAC AGGTTGGAGC CACTCAGGCA GGGAGATTCA GCATCACTCC

2701 . A A P S Y T L K L G E Y G E V T V D C E .
    TGCGGCGCCT TCATACACAC TAAAGCTTGG AGAATATGGA GAGGTGACAG TGGACTGTGA

2761 . P R S G I D T N A Y Y V M T V G T K T F .
    ACCACGGTCA GGGATTGACA CCAATGCATA CTACGTGATG ACTGTTGGAA CAAAGACGTT

2821 . L V H R E W F M D L N L P W S S A G S T .
    CTTGGTCCAT CGTGAGTGGT TCATGGACCT CAACCTCCCT TGGAGCAGTG CTGGAAGTAC

2881 . V W R N R E T L M E F E E P H A T K Q S .
    TGTGTGGAGG AACAGAGAGA CGTTAATGGA GTTTGAGGAA CCACACGCCA CGAAGCAGTC

2941 . V I A L G S Q E G A L H Q A L A G A I P .
    TGTGATAGCA TTGGGCTCAC AAGAGGGAGC TCTGCATCAA GCTTTGGCTG GAGCCATTCC

3001 . V E F S S N T V K L T S G H L K C R V K .
    TGTGGAATTT TCAAGCAACA CTGTCAAGTT GACGTCGGGT CATTTGAAGT GTAGAGTGAA

3061 . M E K L Q L K G T T Y G V C S K A F K F .
    GATGGAAAAA TTGCAGTTGA AGGGAACAAC CTATGGCGTC TGTTCAAAGG CTTTCAAGTT

3121 . L G T P A D T G H G T V V L E L Q Y T G .
    TCTTGGGACT CCCGCAGACA CAGGTCACGG CACTGTGGTG TTGGAATTGC AGTACACTGG

3181 . T D G P C K V P I S S A A S L N D L T P .
    CACGGATGGA CCTTGCAAAG TTCCTATCTC GTCAGCGGCT TCATTGAACG ACCTAACGCC

3241 . V G R L V T V N P F V S V A T A N A K V .
    AGTGGGCAGA TTGGTCACTG TCAACCCTTT TGTTTCAGTG GCCACGGCCA ACGCTAAGGT

3301 . L I E L E P P F G D S Y I V V G R G E Q .
    CCTGATTGAA TTGGAACCAC CCTTTGGAGA CTCATACATA GTGGTGGGCA GAGGAGAACA

3361 . Q I N H H W H K S G S S I G K A F T T T .
    ACAGATCAAT CACCATTGGC ACAAGTCTGG AAGCAGCATT GGCAAAGCCT TTACAACCAC

3421 . L K G A Q R L A A L G D T A W D F G S V .
    CCTCAAAGGA GCGCAGAGAC TAGCCGCTCT AGGAGACACA GCTTGGGACT TTGGATCAGT

3481 . G G V F T S V G K A V H Q V F G G A F R .
    TGGAGGGGTG TTCACCTCAG TTGGGAAGGC TGTCCATCAA GTGTTCGGAG GAGCATTCCG

3541 . S L F G G M S W I T Q G L L G A L L L W .
    CTCACTGTTC GGAGGCATGT CCTGGATAAC GCAAGGATTG CTGGGGGCTC TCCTGTTGTG

3601 . M G I N A R D R S I A L T F L A V G G V .
    GATGGGCATC AATGCTCGTG ATAGGTCCAT AGCTCTCACG TTTCTCGCAG TTGGAGGAGT

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REPLACEMENT SHEET

Figure 4 continued

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      . L L F   L S V N   V H A
3661  TCTGCTCTTC CTCTCCGTGA ACGTGCACGC TTAATTTTTTA TCTAGAGTCG AGTTTTTTATT

      ==> F8L
3721  GACTAGTTAA TCATAAGATA AATAATATAC AGCATTGTAA CCATCGTCAT CCGTTATACG
3781  GGGAAATAATA TTACCATACA GTATTATTAA ATTTTCTTAC GAAGAATATA GATCGGTATT
3841  TATCGTTAGT TTATTTTIACA TTTATTAATT AAACATGTCT ACTATTACCT GTIATGGAAA
3901  TGACAAATTT AGTTATATAA TTTATGATAA AATTAAGATA ATAATATGA AATCAAATAA
3961  TTATGTAAAT GCTACTAGAT TATGTGAATT ACGAGGAAGA AAGTTTACGA ACTGGAAAAA
4021  ATTAAGTGAA TCTAAATAT TAGTCGATAA TGTAAAAAAA ATAAATGATA AAATAAACA
4081  GTTAAAAACG GATATGATTA TATACGTTAA GGATATTGAT CATAAAGGAA GAGATACTTG
4141  CGGTTACTAT GTACACCAAG ATCTGGTATC TTCTATATCA AATTGGATAT CTCCGTTATT
4201  CGCCGTTAAG GTAAATAAAA TTATTTAACTA TTATATATGT AATGAATATG ATATACGACT
4261  TAGCGAAATG GAATCTGATA TGACAGAAGT AATAGATGTA GTTGATAAAT TAGTAGGAGG
4321  ATACAAATGAT GAAATAGCAG AAATAATATA TTTGTTTAAT AAATTTATAG AAAAATATAT
4381  TGCTAACATA TCGTTATCAA CTGAATTTATC TAGTATATTA AATAATTTTA TAAATTTTAA
4441  TAAAAAATAC AATAACGACA TAAAAGATAT TAAATCTTIA ATTCTTGATC TGAAAAACAC
4501  ATCTATAAAA CTAGATAAAA AGTTATTGCA TAAAGATAAT AATGAATCGA ACGATGAAAA
4561  ATTGGAAACA GAAGTTGATA AGCTAATTTT TTTCATCTAA ATAGTATTAT TTTATTGAAG
4621  TACGAAGTTT TACGTTAGAT AAATAATAAA GGTCGATTTT TACTTTGTIA AATATCAAAT
4681  ATGTCATTAT CTGATAAAGA TACAAAAACA CACGGTGATT ATCAACCATC TAACGAACAG
4741  ATATTACAAA AAATACGTCT GACTATGGAA AACGAAGCTG ATAGCCTCAA TAGAAGAAGC
4801  ATTAAAGAAA TTGTTGTAGA TGTTATGAAG AATTGGGATC ATCCTCTCAA CGAAGAAATA
4861  GATAAAGTTC TAAACTGGAA AAATGATACA TTAAACGATT TAGATCATCT AAATACAGAT
4921  GATAATATTA AGGAAATCAT ACAATGTCTG ATTAGAGAAT TTGCGTTTAA AAAGATCAAT
4981  TCTATTATGT ATAGTTATGC TATGGTAAAA CTCAATTCAG ATAACGAAAC ATTGAAAGAT
5041  AAAATTAAGG ATTATTTTAT AGAACTATT CTTAAAGACA AACGTGGTTA TAAACAAAAG
5101  CCATTACCC

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REPLACEMENT SHEET

Figure 8. Nucleotide sequence and translation of the WNV *prM-M-E* region in pSL-5448-1-1, pVR1012 WNV *prM-M-E*.

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      PstI      Kozak      ⇒ WNV capsid leader
1  CTGCAGCCGC CACCATGGGA TCAACCGGAA TTGCAGTCAT GATTGGCCTG ATCGCCAGCG

      ⇒ WNV prM
61  .. G A V T L S N F Q G K V M M T V N A T D .
    TAGGAGCAGT TACCTCTCT AACTTCCAAG GGAAGGTGAT GATGACGGTA AATGCTACTG

121  .. V T D V I T I P T A A G K N L C I V R A .
    ACGTCACAGA TGTCATCACG ATTCCAACAG CTGCTGGAAA GAACCTATGC ATTGTCAGAG

181  .. M D V G Y M C D D T I T Y E C P V L S A .
    CAATGGATGT GGGATACATG TGCATGATA CTATCACTTA TGAATGCCCA GTGCTGTCTGG

241  .. G N D P E D I D C W C T K S A V Y V R Y .
    CTGGTAATGA TCCAGAAGAC ATCGACTGTT GGTGCACAAA GTCAGCAGTC TACGTCAGGT

      ⇒ WNV M
301  .. G R C T K T R H S R R S R R S L T V Q T .
    ATGGAAGATG CACCAAGACA CGCCTACTCA GACGCAGTCG GAGGTCCTG ACAGTGCAGA

361  .. H G E S T L A N K K G A W M D S T K A T .
    CACACGGAGA AAGCACTCTA GCGAACAAGA AGGGGGCTTG GATGGACAGC ACCAAGGCCA

421  .. R Y L V K T E S W I L R N P G Y A L V A .
    CAAGGTATTT GGTAAAAACA GAATCATGGA TCTTGAGGAA CCCTGGATAT GCCCTGGTGG

481  .. A V I G W M L G S N T M Q R V V F V V L .
    CAGCCGTCAT TGGTTGGATG CTTGGGAGCA ACACCATGCA GAGAGTTGTG TTTGTCTGTG

      ⇒ WNV E
541  .. L L L V A P A Y S F N C L G M S N R D F .
    TATTGCTTTT GGTGGCCCCA GCTTACAGCT TCAACTGCCT TGGAATGAGC AACAGAGACT

601  .. L E G V S G A T W V D L V L E G D S C V .
    TCTTGAAGG AGTGTCTGGA GCAACATGGG TGGATTTGGT TCTCGAAGGC GACAGCTGCG

      ClaI
661  .. T I M S K D K P T I D V K M M N M E A A .
    TGACTATCAT GTCTAAGGAC AAGCCTACCA TCGATGTGAA GATGATGAAT ATGGAGGCGG

721  .. N L A E V R S Y C Y L A T V S D L S T K .
    CCAACCTGGC AGAGGTCCGC AGTTATTGCT ATTTGGCTAC CGTCAGCGAT CTCTCCACCA

781  .. A A C P T M G E A H N D K R A D P A F V .
    AAGCTGCGTG CCCGACCATG GGAGAAGCTC ACAATGACAA ACGTGCTGAC CCAGCTTTTG

841  .. C R Q G V V D R G W G N G C G L F G K G .
    TGTGCAGACA AGGAGTGGTG GACAGGGGCT GGGGCAACGG CTGCGGACTA TTTGGCAAAG

901  .. S I D T C A K F A C S T K A I G R T I L .
    GAAGCATTGA CACATGCGCC AAATTTGCCT GCTCTACCAA GGCAATAGGA AGAACCATCT

961  .. K E N I K Y E V A I F V H G P T T V E S .
    TGAAAGAGAA TATCAAGTAC GAAGTGGCCA TTTTGTCCA TGGACCAACT ACTGTGGAGT

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REPLACEMENT SHEET

Figure 8 continued

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1021  .. H G N   Y S T   Q V G A   T Q A   G R F   S I T P .
      CGCACGGAAA CTACTCCACA CAGGTTGGAG CCACTCAGGC AGGGAGATTC AGCATCACTC

1081  .. A A P   S Y T   L K L G   E Y G   E V T   V D C E .
      CTGCGGCGCC TTCATACACA CTAAAGCTTG GAGAATATGG AGAGGTGACA GTGGACTGTG

1141  .. P R S   G I D   T N A Y   Y V M   T V G   T K T F .
      AACCACGGTC AGGGATTGAC ACCAATGCAT ACTACGTGAT GACTGTTGGA ACAAAGACGT

1201  .. L V H   R E W   F M D L   N L P   W S S   A G S T .
      TCTTGGTCCA TCGTGAGTGG TTCATGGACC TCAACCTCCC TTGGAGCAGT GCTGGAAGTA

1261  .. V W R   N R E   T L M E   F E E   F H A   T K Q S .
      CTGTGTGGAG GAACAGAGAG ACGTTAATGG AGTTTGAGGA ACCACACGCC ACGAAGCAGT

1321  .. V I A   L G S   Q E G A   L H Q   A L A   G A I P .
      CTGTGATAGC ATTGGGCTCA CAAGAGGGAG CTCTGCATCA AGCTTTGGCT GGAGCCATTC

1381  .. V E F   S S N   T V K L   T S G   H L K   C R V K .
      CTGTGGAATT TTCAAGCAAC ACTGTCAAGT TGACGTCGGG TCATTTGAAG TGTAGAGTGA

1441  .. M E K   L Q L   K G T T   Y G V   C S K   A F K F .
      AGATGGAAAA ATTGCAGTTG AAGGGAACAA CCTATGGCGT CTGTTCAAAG GCTTTCAAGT

1501  .. L G T   P A D   T G H G   T V V   L E L   Q Y T G .
      TTCTTGGGAC TCCCGCAGAC ACAGGTCACG GCACTGTGGT GTTGAATTG CAGTACACTG

1561  .. T D G   P C K   V P I S   S A A   S L N   D L T P .
      GCACGGATGG ACCTTGCAAA GTTCCTATCT CGTCAGCGGC TTCATTGAAC GACCTAACGC

1621  .. V G R   L V T   V N P F   V S V   A T A   N A K V .
      CAGTGGGCAG ATTGGTCACT GTCAACCCTT TTGTTTCAGT GGCCACGGCC AACGCTAAGG

1681  .. L I E   L E P   P F G D   S Y I   V V G   R G E Q .
      TCCTGATTGA ATTGGAACCA CCCTTTGGAG ACTCATACAT AGTGGTGGGC AGAGGAGAAC

1741  .. Q I N   H H W   H K S G   S S I   G K A   F T T T .
      AACAGATCAA TCACCATTGG CACAAGTCTG GAAGCAGCAT TGGCAAAGCC TTTACAACCA

1801  .. L K G   A Q R   L A A L   G D T   A W D   F G S V .
      CCCTCAAAGG AGCGCAGAGA CTAGCCGCTC TAGGAGACAC AGCTTGGGAC TTTGGATCAG

1861  .. G G V   F T S   V G K A   V H Q   V F G   G A F R .
      TTGGAGGGGT GTTCACCTCA GTTGGGAAGG CTGTCCATCA AGTGTTTCGA GGAGCATTC

1921  .. S L F   G G M   S W I T   Q G L   L G A   L L L W .
      GCTCACTGTT CGGAGGCATG TCCTGGATAA CGCAAGGATT GCTGGGGGCT CTCCTGTTGT

1981  .. M G I   N A R   D R S I   A L T   F L A   V G G V .
      GGATGGGCAT CAATGCTCGT GATAGGTCCA TAGCTCTCAC GTTTCTCGCA GTTGGAGGAG

2041  .. L L F   L S V   N V H A
      TTCTGCTCTT CCTCTCCGTG AACGTGCACG CTTAATTTTT A[TCTAGA]

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XbaI

REPLACEMENT SHEET

FIGURE 9

Sequence of pDS-2946-1-1, pC5 H6p WNV *prM-M-E*.

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1   GCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTTCATTAATGCAGCTGGCA
61  CGACAGGTTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAACGCAATTAATGTGAGTTAGCT
121 CACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTCCGGCTCGTATGTTGTGTGGAAT
181 TGTGAGCGGATAACAATTTACACAGGAAACAGCTATGACCATGATTACGAATTGCGGCC      => C5R
241 GCAATTCTGAATGTTAAATGTTATACTTTGGATGAAGCTATAAAATATGCATTGGAAAAAT
301 AATCCATTTAAAGAAAGGATTCAAATACTACAAAACCTAAGCGATAATATGTTAACTAAG
361 CTTATTCTTAAACGACGCTTTAAATATACACAAATAAACATAATTTTTGTATAACCTAACA
421 AATAACTAAAACATAAAAAATAATAAAGGAAATGTAATATCGTAATTATTTTACTCAGGA
481 ATGGGGTTAAATATTTATATCACGTGTATATCTATACTGTTATCGTATACTCTTTACAAT
541 TACTATTACGAATATGCAAGAGATAATAAGATTACGTATTTAAGAGAATCTTGTCATGAT
601 AATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGTTACATAAAGTCAGTTGGAAA
661 GATGGATTTGACAGATGTAACCTTAATAGGTGCAAAAATGTTAAATAACAGCATTCTATCG
721 GAAGATAGGATACCACTTATATTATACAAAAATCACTGGTTGGATAAAACAGATTCTGCA
781 ATATTCGTAAAAGATGAAGATTACTGCGAATTTGTAACTATGACAATAAAAAGCCATTT
841 ATCTCAACGACATCGTGTAATTTCTCCATGTTTTATGTATGTGTTTCAGATATTATGAGA
901 TTACTATAAACTTTTTGTATACTTATATTCGTAACTATATTAATCATGAAGAAAATGA
961 AAAAGTATAGAAGCTGTTACGAGCGGTTGTTGAAAACAACAAAATTATACATTCAAGAT
1021 GGCTTACATATACGTCTGTGAGGCTATCATGGATAATGACAATGCATCTCTAAATAGGTT
1081 TTTGGACAATGGATTGACCCCTAACACGGAATATGGTACTCTACAATCTCCTCTTGAAAT
1141 GGCTGTAATGTTCAAGAATACCGAGGCTATAAAAAATCTTGATGAGGTATGGAGCTAAACC
1201 TGTAGTTACTGAATGCACAACTTCTGTCTGCATGATGCGGTGTTGAGAGACGACTACAA
1261 AATAGTGAAAGATCTGTTGAAGAATAACTATGTAAACAATGTTCTTTACAGCGGAGGCTT
1321 TACTCCTTTGTGTTTGGCAGCTTACCTTAACAAAGTTAATTTGGTTAAACTTCTATTGGC
1381 TCATTGGGCGGATGTAGATATTTCAAACACGGATCGGTTAACTCCTCTACATATAGCCGT
1441 ATCAAATAAAAAATTTAACAATGGTTAACTTCTATTGAACAAAGGTGCTGATACTGACTT
1501 GCTGGATAACATGGGATGTACTCCTTTAATGATCGCTGTACAATCTGGAAATATTGAAAT
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REPLACEMENT SHEET

Figure 9 continued

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1561  ATGTAGCACACTACTTAAAAAAATAAAATGTCCAGAACTGGGAAAAATTGATCTTGCCA

1621  GCTGTAATTCATGGTAGAAAAGAAGTGCTCAGGCTACTTTTCAACAAAGGAGCAGATGTA

1681  AACTACATCTTTGAAAGAAATGGAAAAATCATATACTGTTTTGGAATTGATTAAAGAAAGT

1741  TACTCTGAGACACAAAAGAGGTAGCTGAAGTGGTACTCTCAAAGGTACGTGACTAATTAG

1801  CTATAAAAAGGATCCGGGTAAATTAATTAGTCATCAGGCAGGGCGAGAACGAGACTATCT

                                     => H6p
1861  GCTCGTTAATTAATTAGAGCTTCTTTATTCTATACTTAAAAAGTGAAAATAAATACAAAG
1921  GTTCTTGAGGGTTGTGTTAAATTGAAAGCGAGAAATAATCATAAATTATTTTATTATCGC

                                     => WNV capsid leader
                                     M T G I A V M I G L I A
1981  GATATCCGTTAAGTTTGTATCGTAATGACCGGAATTGCAGTCATGATTGGCCTGATCGCC

                                     => WNV prM start
                                     S V G A V T L S N F Q G K V M M T V N A
2041  AGCGTAGGAGCGGTTACCCTCTCTAACTTCCAAGGAAGGTGATGATGACGGTAAATGCT

                                     T D V T D V I T I P T A A G K N L C I V
2101  ACTGACGTCACAGATGTCATCACGATTCCAACAGCTGCTGGAAAGAACCTATGCATTGTC

                                     R A M D V G Y M C D D T I T Y E C P V L
2161  AGAGCAATGGATGTGGGATACATGTGCGATGATACTATCACTTATGAATGCCAGTGCTG

                                     S A G N D P E D I D C W C T K S A V Y V
2221  TCGGCTGGTAATGATCCAGAAGACATCGACTGTTGGTGCACAAAGTCAGCAGTCTACGT

                                     => WNV M start
                                     R Y G R C T K T R H S R R S R R S L T V
2281  AGGTATGGAAGATGCACCAAGACACGCCACTCAAGACGCAGTCGGAGGTCACTGACAGTG

                                     Q T H G E S T L A N K K G A W M D S T K
2341  CAGACACACGGAGAAAGCACTCTAGCGAACAAGAAGGGGGCTTGATGGACAGCACCAAG

                                     A T R Y L V K T E S W I L R N P G Y A L
2401  GCCACAAGGTATTTGGTAAAAACAGAATCATGGATCTTGAGGAACCCTGGATATGCCCTG

                                     V A A V I G W M L G S N T M Q R V V F V
2461  GTGGCAGCCGTCATTGGTTGGATGCTTGGGAGCAACACCATGCAGAGAGTTGTGTTTGTC

                                     => WNV E start
                                     V L L L L V A P A Y S F N C L G M S N R
2521  GTGCTATTGCTTTTGGTGGCCCCAGCTTACAGCTTCAACTGCCTTGGAATGAGCAACAGA

                                     D F L E G V S G A T W V D L V L E G D S
2581  GACTTCTTGGAAGGAGTGTCTGGAGCAACATGGGTGGATTGTTCTCGAAGGCGACAGC

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REPLACEMENT SHEET

Figure 9 continued

2641 C V T I M S K D K P T I D V K M M N M E
 T G C G T G A C T A T C A T G T C T A A G G A C A A G C C T A C C A T C G A T G T G A A G A T G A T G A A T A T G G A G

2701 A A N L A E V R S Y C Y L A T V S D L S
 G C G G C C A A C C T G G C A G A G G T C C G C A G T T A T T G C T A T T T G G C T A C C G T C A G C G A T C T C T C C

2761 T K A A C P T M G E A H N D K R A D P A
 A C C A A A G C T G C G T G C C C G A C C A T G G G A G A A G C T C A C A A T G A C A A C G T G C T G A C C C A G C T

2821 F V C R Q G V V D R G W G N G C G L F G
 T T T G T G T G C A G A C A A G G A G T G G T G G A C A G G G G C T G G G G C A A C G G C T G C G G A C T A T T T G G C

2881 K G S I D T C A K F A C S T K A I G R T
 A A A G G A A G C A T T G A C A C A T G C G C C A A A T T T G C C T G C T C T A C C A A G G C A A T A G G A A G A A C C

2941 I L K E N I K Y E V A I F V H G P T T V
 A T C T T G A A A G A G A A T A T C A A G T A C G A A G T G G C C A T C T T C G T G C A C G G A C C A A C T A C T G T G
 mutated T5NT

3001 E S H G N Y S T Q V G A T Q A G R F S I
 G A G T C G C A C G G A A A C T A C T C C A C A C A G G T T G G A G C C A C T C A G G C A G G G A G A T T C A G C A T C

3061 T P A A P S Y T L K L G E Y G E V T V D
 A C T C C T G C G G C G C C T T C A T A C A C A C T A A A G C T T G G A G A A T A T G G A G A G G T G A C A G T G G A C

3121 C E P R S G I D T N A Y Y V M T V G T K
 T G T G A A C C A C G G T C A G G G A T T G A C A C C A A T G C A T A C T A C G T G A T G A C T G T T G G A A C A A A G

3181 T F L V H R E W F M D L N L P W S S A G
 A C G T T C T T G G T C C A T C G T G A G T G G T T C A T G G A C C T C A A C C T C C C T T G G A G C A G T G C T G G A

3241 S T V W R N R E T L M E F E E P H A T K
 A G T A C T G T G T G G A G G A A C A G A G A C G T T A A T G G A G T T T G A G G A A C C A C A C G C C A C G A A G

3301 Q S V I A L G S Q E G A L H Q A L A G A
 C A G T C T G T G A T A G C A T T G G G C T C A C A A G A G G G A G C T C T G C A T C A A G C T T T G G C T G G A G C C

3361 I P V E F S S N T V K L T S G H L K C R
 A T T C C T G T G G A A T T T T C A A G C A A C A C T G T C A A G T T G A C G T C G G G T C A T T T G A A G T G T A G A

3421 V K M E K L Q L K G T T Y G V C S K A F
 G T G A A G A T G G A A A A T T G C A G T T G A A G G G A A C A C C T A T G G C G T C T G T T C A A A G G C T T T C

3481 K F L G T P A D T G H G T V V L E L Q Y
 A A G T T T C T T G G G A C T C C C G C A G A C A C A G G T C A C G G C A C T G T G G T G T T G G A A T T G C A G T A C

3541 T G T D G P C K V P I S S A A S L N D L
 A C T G G C A C G G A T G G A C C T T G C A A A G T T C C T A T C T C G T C A G C G G C T T C A T T G A A C G A C C T A

3601 T P V G R L V T V N P F V S V A T A N A
 A C G C C A G T G G G C A G A T T G G T C A C T G T C A A C C C T T T T G T T T C A G T G G C C A C G G C C A A C G C T

3661 K V L I E L E P P F G D S Y I V V G R G
 A A G G T C C T G A T T G A A T T G G A A C C A C C C T T T G G A G A C T C A T A C A T A G T G G T G G G C A G A G G A

REPLACEMENT SHEET

Figure 9 continued

3721 E Q Q I N H H W H K S G S S I G K A F T
GAACAACAGATCAATCACCATTGGCACAAGTCTGGAAGCAGCATTGGCAAAGCCTTTACA

3781 T T L K G A Q R L A A L G D T A W D F G
ACCACCCTCAAAGGAGCGCAGAGACTAGCCGCTCTAGGAGACACAGCTTGGGACTTTGGA

3841 S V G G V F T S V G K A V H Q V F G G A
TCAGTTGGAGGGGTGTTACCTCAGTTGGGAAGGCTGTCCATCAAGTGTTCGGAGGAGCA

3901 F R S L F G G M S W I T Q G L L G A L L
TTCCGCTCACTGTTTCGGAGGCATGTCCTGGATAACGCAAGGATTGCTGGGGGCTCTCCTG

3961 L W M G I N A R D R S I A L T F L A V G
TTGTGGATGGGCATCAATGCTCGTGATAGGTCCATAGCTCTCACGTTTCTCGCAGTTGGA

⇒ C5L

4021 G V L L F L S V N V H A *
GGAGTTCTGCTCTTCTCTCCGTGAACGTGCACGCTTAATTTTTATCTAGAATCGATCCC

4081 GGGTTTTTATGACTAGTTAATCACGGCCGCTTATAAAGATCTAAAATGCATAATTTCTAA

4141 ATAATGAAAAAAGTACATCATGAGCAACGCGTTAGTATATTTTACAATGGGAGATTAAAG

4201 CTCTATACCGTTCTATGTTTATTGATTAGATGATGTTTTAGAAAAAGAAAGTTATTGAAT

4261 ATGAAAACTTTAAATGAAGATGAAGATGACGACGATGATTATTGTTGTAAATCTGTTTTAG

4321 ATGAAGAAGATGACGCGCTAAAGTATACTATGGTTACAAAGTATAAGTCTATACTACTAA

4381 TGGCGACTTGTGCAAGAAGGTATAGTATAGTGAAAATGTTGTTAGATTATGATTATGAAA

4441 AACCAAATAAATCAGATCCATATCTAAAGGTATCTCCTTTGCACATAATTTTCATCTATTC

4501 CTAGTTTAGAATACTGACGCCAAGCTTGGCACTGGCCGTCGTTTTACAACGTCGTGACT

4561 GGGAAAACCTGGCGTTACCCAACTTAATCGCCTTGACGACATCCCCCTTTGCGCAGCT

4621 GGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCAGCCTGAATG

4681 GCGAATGGCGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTACACCGCA

4741 TATGGTGCACTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGCCCCGACACC

4801 CGCCAACACCCGCTGACGCGCCCTGACGGGCTTGTCTGCTCCCGGCATCCGCTTACAGAC

4861 AAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAGGTTTTACCGTCATCACCAGAAAC

4921 GCGCGAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAA

4981 TGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTT

5041 TATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGC

5101 TTCAATAATATTGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTC

REPLACEMENT SHEET

Figure 9 continued

5161 CCTTTTTTGC GG CATTTTGCCTTCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAA
5221 AAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCG
5281 GTAAGATCCTTGAGAGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAG
5341 TTCTGCTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCC
5401 GCATACACTATTCTCAGAATGACTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTA
5461 CGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCCATAACCATGAGTGATAAACTG
5521 CGGCCAACTTACTTCTGACAACGATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACA
5581 ACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATAC
5641 CAAACGACGAGCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAATAT
5701 TAACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGG
5761 ATAAAGTTGCAGGACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGGTTTATTGCTGATA
5821 AATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTA
5881 AGCCCTCCCGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAA
5941 ATAGACAGATCGCTGAGATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAG
6001 TTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAGGATCTAGG
6061 TGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCTGTTCCACT
6121 GAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCG
6181 TAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTGTGTTGCCGGATC
6241 AAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATA
6301 CTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTA
6361 CATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTC
6421 TTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGG
6481 GGGGTTCTGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTAC
6541 AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGG
6601 TAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAACGCCTGGT
6661 ATCTTTATAGTCCTGTGCGGTTTTGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCT
6721 CGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGG
6781 CCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCTGATTCTGTGGATA

REPLACEMENT SHEET

Figure 9 continued

6841 ACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCA

6901 GCGAGTCAGTGAGCGAGGAAGCGGAAGA

REPLACEMENT SHEET

FIGURE 12

agtagttcgc ctgtgtgagc tgacaaactt agtagtgttt gtgaggatta acaacaatta
60

acacagtgcg agctgtttct tagcacgaag atctcg atg tct aag aaa cca gga
114

Met Ser Lys Lys Pro Gly
1 5

ggg ccc ggc aag agc cgg gct gtc aat atg cta aaa cgc gga atg ccc
162

Gly Pro Gly Lys Ser Arg Ala Val Asn Met Leu Lys Arg Gly Met Pro
10 15 20

cgc gtg ttg tcc ttg att gga ctg aag agg gct atg ttg agc ctg atc
210

Arg Val Leu Ser Leu Ile Gly Leu Lys Arg Ala Met Leu Ser Leu Ile
25 30 35

gac ggc aag ggg cca ata cga ttt gtg ttg gct ctc ttg gcg ttc ttc
258

Asp Gly Lys Gly Pro Ile Arg Phe Val Leu Ala Leu Leu Ala Phe Phe
40 45 50

agg ttc aca gca att gct ccg acc cga gca gtg ctg gat cga tgg aga
306

Arg Phe Thr Ala Ile Ala Pro Thr Arg Ala Val Leu Asp Arg Trp Arg
55 60 65 70

ggt gtg aac aaa caa aca gcg atg aaa cac ctt ctg agt ttt aag aag
354

Gly Val Asn Lys Gln Thr Ala Met Lys His Leu Leu Ser Phe Lys Lys
75 80 85

gaa cta ggg acc ttg acc agt gct atc aat cgg cgg agc tca aaa caa
402

Glu Leu Gly Thr Leu Thr Ser Ala Ile Asn Arg Arg Ser Ser Lys Gln
90 95 100

aag aaa aga gga gga aag acc gga att gca gtc atg att ggc ctg atc
450

Lys Lys Arg Gly Gly Lys Thr Gly Ile Ala Val Met Ile Gly Leu Ile
105 110 115

gcc agc gta gga gca gtt acc ctc tct aac ttc caa ggg aag gtg atg
498

Ala Ser Val Gly Ala Val Thr Leu Ser Asn Phe Gln Gly Lys Val Met
120 125 130

REPLACEMENT SHEET

Figure 12 continued

atg acg gta aat gct act gac gtc aca gat gtc atc acg att cca aca	
546	
Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr Ile Pro Thr	
135	140 145 150
gct gct gga aag aac cta tgc att gtc aga gca atg gat gtg gga tac	
594	
Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp Val Gly Tyr	
	155 160 165
atg tgc gat gat act atc act tat gaa tgc cca gtg ctg tcg gct ggt	
642	
Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu Ser Ala Gly	
	170 175 180
aat gat cca gaa gac atc gac tgt tgg tgc aca aag tca gca gtc tac	
690	
Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser Ala Val Tyr	
	185 190 195
gtc agg tat gga aga tgc acc aag aca cgc cac tca aga cgc agt cgg	
738	
Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg Arg Ser Arg	
	200 205 210
agg tca ctg aca gtg cag aca cac gga gaa agc act cta gcg aac aag	
786	
Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu Ala Asn Lys	
215	220 225 230
aag ggg gct tgg atg gac agc acc aag gcc aca agg tat ttg gta aaa	
834	
Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr Leu Val Lys	
	235 240 245
aca gaa tca tgg atc ttg agg aac cct gga tat gcc ctg gtg gca gcc	
882	
Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu Val Ala Ala	
	250 255 260
gtc att ggt tgg atg ctt ggg agc aac acc atg cag aga gtt gtg ttt	
930	
Val Ile Gly Trp Met Leu Gly Ser Asn Thr Met Gln Arg Val Val Phe	
	265 270 275
gtc gtg cta ttg ctt ttg gtg gcc cca gct tac agc ttc aac tgc ctt	
978	
Val Val Leu Leu Leu Leu Val Ala Pro Ala Tyr Ser Phe Asn Cys Leu	
	280 285 290

REPLACEMENT SHEET

Figure 12 continued

gga atg agc aac aga gac ttc ttg gaa gga gtg tct gga gca aca tgg	
1026	
Gly Met Ser Asn Arg Asp Phe Leu Glu Gly Val Ser Gly Ala Thr Trp	
295	300 305 310
gtg gat ttg gtt ctc gaa ggc gac agc tgc gtg act atc atg tct aag	
1074	
Val Asp Leu Val Leu Glu Gly Asp Ser Cys Val Thr Ile Met Ser Lys	
	315 320 325
gac aag cct acc atc gat gtg aag atg atg aat atg gag gcg gcc aac	
1122	
Asp Lys Pro Thr Ile Asp Val Lys Met Met Asn Met Glu Ala Ala Asn	
	330 335 340
ctg gca gag gtc cgc agt tat tgc tat ttg gct acc gtc agc gat ctc	
1170	
Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu Ala Thr Val Ser Asp Leu	
	345 350 355
tcc acc aaa gct gcg tgc ccg acc atg gga gaa gct cac aat gac aaa	
1218	
Ser Thr Lys Ala Ala Cys Pro Thr Met Gly Glu Ala His Asn Asp Lys	
	360 365 370
cgt gct gac cca gct ttt gtg tgc aga caa gga gtg gtg gac agg ggc	
1266	
Arg Ala Asp Pro Ala Phe Val Cys Arg Gln Gly Val Val Asp Arg Gly	
375	380 385 390
tgg ggc aac ggc tgc gga cta ttt ggc aaa gga agc att gac aca tgc	
1314	
Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys	
	395 400 405
gcc aaa ttt gcc tgc tct acc aag gca ata gga aga acc atc ttg aaa	
1362	
Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile Gly Arg Thr Ile Leu Lys	
	410 415 420
gag aat atc aag tac gaa gtg gcc att ttt gtc cat gga cca act act	
1410	
Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val His Gly Pro Thr Thr	
	425 430 435
gtg gag tcg cac gga aac tac tcc aca cag gtt gga gcc act cag gca	
1458	
Val Glu Ser His Gly Asn Tyr Ser Thr Gln Val Gly Ala Thr Gln Ala	
	440 445 450

REPLACEMENT SHEET

Figure 12 continued

ggg aga ttc agc atc act cct gcg gcg cct tca tac aca cta aag ctt	
1506	
Gly Arg Phe Ser Ile Thr Pro Ala Ala Pro Ser Tyr Thr Leu Lys Leu	
455	460 465 470
gga gaa tat gga gag gtg aca gtg gac tgt gaa cca cgg tca ggg att	
1554	
Gly Glu Tyr Gly Glu Val Thr Val Asp Cys Glu Pro Arg Ser Gly Ile	
	475 480 485
gac acc aat gca tac tac gtg atg act gtt gga aca aag acg ttc ttg	
1602	
Asp Thr Asn Ala Tyr Tyr Val Met Thr Val Gly Thr Lys Thr Phe Leu	
	490 495 500
gtc cat cgt gag tgg ttc atg gac ctc aac ctc cct tgg agc agt gct	
1650	
Val His Arg Glu Trp Phe Met Asp Leu Asn Leu Pro Trp Ser Ser Ala	
	505 510 515
gga agt act gtg tgg agg aac aga gag acg tta atg gag ttt gag gaa	
1698	
Gly Ser Thr Val Trp Arg Asn Arg Glu Thr Leu Met Glu Phe Glu Glu	
	520 525 530
cca cac gcc acg aag cag tct gtg ata gca ttg ggc tca caa gag gga	
1746	
Pro His Ala Thr Lys Gln Ser Val Ile Ala Leu Gly Ser Gln Glu Gly	
535	540 545 550
gct ctg cat caa gct ttg gct gga gcc att cct gtg gaa ttt tca agc	
1794	
Ala Leu His Gln Ala Leu Ala Gly Ala Ile Pro Val Glu Phe Ser Ser	
	555 560 565
aac act gtc aag ttg acg tcg ggt cat ttg aag tgt aga gtg aag atg	
1842	
Asn Thr Val Lys Leu Thr Ser Gly His Leu Lys Cys Arg Val Lys Met	
	570 575 580
gaa aaa ttg cag ttg aag gga aca acc tat ggc gtc tgt tca aag gct	
1890	
Glu Lys Leu Gln Leu Lys Gly Thr Thr Tyr Gly Val Cys Ser Lys Ala	
	585 590 595
ttc aag ttt ctt ggg act ccc gca gac aca ggt cac ggc act gtg gtg	
1938	
Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr Gly His Gly Thr Val Val	
	600 605 610

REPLACEMENT SHEET

Figure 12 continued

ttg gaa ttg cag tac act ggc acg gat gga cct tgc aaa gtt cct atc	
1986	
Leu Glu Leu Gln Tyr Thr Gly Thr Asp Gly Pro Cys Lys Val Pro Ile	
615	620 625 630
tcg tca gtg gct tca ttg aac gac cta acg cca gtg ggc aga ttg gtc	
2034	
Ser Ser Val Ala Ser Leu Asn Asp Leu Thr Pro Val Gly Arg Leu Val	
	635 640 645
act gtc aac cct ttt gtt tca gtg gcc acg gcc aac gct aag gtc ctg	
2082	
Thr Val Asn Pro Phe Val Ser Val Ala Thr Ala Asn Ala Lys Val Leu	
	650 655 660
att gaa ttg gaa cca ccc ttt gga gac tca tac ata gtg gtg ggc aga	
2130	
Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser Tyr Ile Val Val Gly Arg	
	665 670 675
gga gaa caa cag atc aat cac cat tgg cac aag tct gga agc agc att	
2178	
Gly Glu Gln Gln Ile Asn His His Trp His Lys Ser Gly Ser Ser Ile	
	680 685 690
ggc aaa gcc ttt aca acc acc ctc aaa gga gcg cag aga cta gcc gct	
2226	
Gly Lys Ala Phe Thr Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala	
695	700 705 710
cta gga gac aca gct tgg gac ttt gga tca gtt gga ggg gtg ttc acc	
2274	
Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly Val Phe Thr	
	715 720 725
tca gtt ggg aag gct gtc cat caa gtg ttc gga gga gca ttc cgc tca	
2322	
Ser Val Gly Lys Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Ser	
	730 735 740
ctg ttc gga ggc atg tcc tgg ata acg caa gga ttg ctg ggg gct ctc	
2370	
Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu Gly Ala Leu	
	745 750 755
ctg ttg tgg atg ggc atc aat gct cgt gat agg tcc ata gct ctc acg	
2418	
Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile Ala Leu Thr	
	760 765 770

REPLACEMENT SHEET

Figure 12 continued

ttt	ctc	gca	gtt	gga	gga	gtt	ctg	ctc	ttc	ctc	tcc	gtg	aac	gtg	cac	
2466																
Phe	Leu	Ala	Val	Gly	Gly	Val	Leu	Leu	Phe	Leu	Ser	Val	Asn	Val	His	
775					780					785					790	
gct	gac	act	ggg	tgt	gcc	ata	gac	atc	agc	cgg	caa	gag	ctg	aga	tgt	
2514																
Ala	Asp	Thr	Gly	Cys	Ala	Ile	Asp	Ile	Ser	Arg	Gln	Glu	Leu	Arg	Cys	
				795					800					805		
gga	agt	gga	gtg	ttc	ata	cac	aat	gat	gtg	gag	gct	tgg	atg	gac	cgg	
2562																
Gly	Ser	Gly	Val	Phe	Ile	His	Asn	Asp	Val	Glu	Ala	Trp	Met	Asp	Arg	
			810					815					820			
tac	aag	tat	tac	cct	gaa	acg	cca	caa	ggc	cta	gcc	aag	atc	att	cag	
2610																
Tyr	Lys	Tyr	Tyr	Pro	Glu	Thr	Pro	Gln	Gly	Leu	Ala	Lys	Ile	Ile	Gln	
			825				830					835				
aaa	gct	cat	aag	gaa	gga	gtg	tgc	ggc	cta	cga	tca	gtt	tcc	aga	ctg	
2658																
Lys	Ala	His	Lys	Glu	Gly	Val	Cys	Gly	Leu	Arg	Ser	Val	Ser	Arg	Leu	
	840					845					850					
gag	cat	caa	atg	tgg	gaa	gca	gtg	aag	gac	gag	ctg	aac	act	ctt	ttg	
2706																
Glu	His	Gln	Met	Trp	Glu	Ala	Val	Lys	Asp	Glu	Leu	Asn	Thr	Leu	Leu	
855					860					865					870	
aag	gag	aat	ggc	gtg	gac	ctt	agt	gtc	gtg	gtt	gag	aaa	cag	gag	gga	
2754																
Lys	Glu	Asn	Gly	Val	Asp	Leu	Ser	Val	Val	Val	Glu	Lys	Gln	Glu	Gly	
				875					880					885		
atg	tac	aag	tca	gca	cct	aaa	cgc	ctc	acc	gcc	acc	acg	gaa	aaa	ttg	
2802																
Met	Tyr	Lys	Ser	Ala	Pro	Lys	Arg	Leu	Thr	Ala	Thr	Thr	Glu	Lys	Leu	
			890					895					900			
gaa	att	ggc	tgg	aag	gcc	tgg	gga	aag	agt	att	tta	ttt	gca	cca	gaa	
2850																
Glu	Ile	Gly	Trp	Lys	Ala	Trp	Gly	Lys	Ser	Ile	Leu	Phe	Ala	Pro	Glu	
		905					910					915				
ctc	gcc	aac	aac	acc	ttt	gtg	gtt	gat	ggc	ccg	gag	acc	aag	gaa	tgt	
2898																
Leu	Ala	Asn	Asn	Thr	Phe	Val	Val	Asp	Gly	Pro	Glu	Thr	Lys	Glu	Cys	
	920					925					930					

REPLACEMENT SHEET

Figure 12 continued

cgc act cag aat cgc gct tgg aat agc tta gaa gtg gag gat ttt gga
2946

Pro Thr Gln Asn Arg Ala Trp Asn Ser Leu Glu Val Glu Asp Phe Gly
935 940 945 950

ttt ggt ctc acc agc act cgg atg ttc ctg aag gtc aga gag agc aac
2994

Phe Gly Leu Thr Ser Thr Arg Met Phe Leu Lys Val Arg Glu Ser Asn
955 960 965

aca act gaa tgt gac tcg aag atc att gga acg gct gtc aag aac aac
3042

Thr Thr Glu Cys Asp Ser Lys Ile Ile Gly Thr Ala Val Lys Asn Asn
970 975 980

ttg gcg atc cac agt gac ctg tcc tat tgg att gaa agc agg ctc aat
3090

Leu Ala Ile His Ser Asp Leu Ser Tyr Trp Ile Glu Ser Arg Leu Asn
985 990 995

gat acg tgg aag ctt gaa agg gca gtt ctg ggt gaa gtc aaa tca
3135

Asp Thr Trp Lys Leu Glu Arg Ala Val Leu Gly Glu Val Lys Ser
1000 1005 1010

tgt acg tgg cct gag acg cat acc ttg tgg ggc gat gga atc ctt
3180

Cys Thr Trp Pro Glu Thr His Thr Leu Trp Gly Asp Gly Ile Leu
1015 1020 1025

gag agt gac ttg ata ata cca gtc aca ctg gcg gga cca cga agc
3225

Glu Ser Asp Leu Ile Ile Pro Val Thr Leu Ala Gly Pro Arg Ser
1030 1035 1040

aat cac aat cgg aga cct ggg tac aag aca caa aac cag ggc cca
3270

Asn His Asn Arg Arg Pro Gly Tyr Lys Thr Gln Asn Gln Gly Pro
1045 1050 1055

tgg gac gaa ggc cgg gta gag att gac ttc gat tac tgc cca gga
3315

Trp Asp Glu Gly Arg Val Glu Ile Asp Phe Asp Tyr Cys Pro Gly
1060 1065 1070

act acg gtc acc ctg agt gag agc tgc gga cac cgt gga cct gcc
3360

Thr Thr Val Thr Leu Ser Glu Ser Cys Gly His Arg Gly Pro Ala
1075 1080 1085

REPLACEMENT SHEET

Figure 12 continued

act cgc acc acc aca gag agc gga aag ttg ata aca gat tgg tgc
3405

Thr Arg Thr Thr Thr Glu Ser Gly Lys Leu Ile Thr Asp Trp Cys
1090 1095 1100

tgc agg agc tgc acc tta cca cca ctg cgc tac caa act gac agc
3450

Cys Arg Ser Cys Thr Leu Pro Pro Leu Arg Tyr Gln Thr Asp Ser
1105 1110 1115

ggc tgt tgg tat ggt atg gag atc aga cca cag aga cat gat gaa
3495

Gly Cys Trp Tyr Gly Met Glu Ile Arg Pro Gln Arg His Asp Glu
1120 1125 1130

aag acc ctc gtg cag tca caa gtg aat gct tat aat gct gat atg
3540

Lys Thr Leu Val Gln Ser Gln Val Asn Ala Tyr Asn Ala Asp Met
1135 1140 1145

att gac cct ttt cag ttg ggc ctt ctg gtc gtg ttc ttg gcc acc
3585

Ile Asp Pro Phe Gln Leu Gly Leu Leu Val Val Phe Leu Ala Thr
1150 1155 1160

cag gag gtc ctt cgc aag agg tgg aca gcc aag atc agc atg cca
3630

Gln Glu Val Leu Arg Lys Arg Trp Thr Ala Lys Ile Ser Met Pro
1165 1170 1175

gct ata ctg att gct ctg cta gtc ctg gtg ttt ggg ggc att act
3675

Ala Ile Leu Ile Ala Leu Leu Val Leu Val Phe Gly Gly Ile Thr
1180 1185 1190

tac act gat gtg tta cgc tat gtc atc ttg gtg ggg gca gct ttc
3720

Tyr Thr Asp Val Leu Arg Tyr Val Ile Leu Val Gly Ala Ala Phe
1195 1200 1205

gca gaa tct aat tcg gga gga gac gtg gta cac ttg gcg ctc atg
3765

Ala Glu Ser Asn Ser Gly Gly Asp Val Val His Leu Ala Leu Met
1210 1215 1220

gcg acc ttc aag ata caa cca gtg ttt atg gtg gca tcg ttt ctg
3810

Ala Thr Phe Lys Ile Gln Pro Val Phe Met Val Ala Ser Phe Leu
1225 1230 1235

REPLACEMENT SHEET

Figure 12 continued

aaa gcg	aga tgg	acc aac	cag	gag aac	att ttg	ttg	atg ttg	gcg						
3855														
Lys	Ala	Arg	Trp	Thr	Asn	Gln	Glu	Asn	Ile	Leu	Leu	Met	Leu	Ala
	1240					1245					1250			
gct gtt	ttc ttt	caa atg	gct	tat cac	gat gcc	cgc	caa att	ctg						
3900														
Ala	Val	Phe	Phe	Gln	Met	Ala	Tyr	His	Asp	Ala	Arg	Gln	Ile	Leu
	1255					1260					1265			
ctc tgg	gag atc	cct gat	gtg	ttg aat	tca ctg	gcg	gta gct	tgg						
3945														
Leu	Trp	Glu	Ile	Pro	Asp	Val	Leu	Asn	Ser	Leu	Ala	Val	Ala	Trp
	1270					1275					1280			
atg ata	ctg aga	gcc ata	aca	ttc aca	acg aca	tca	aac gtg	gtt						
3990														
Met	Ile	Leu	Arg	Ala	Ile	Thr	Phe	Thr	Thr	Thr	Ser	Asn	Val	Val
	1285					1290					1295			
gtt ccg	ctg cta	gcc ctg	cta	aca ccc	ggg ctg	aga	tgc ttg	aat						
4035														
Val	Pro	Leu	Leu	Ala	Leu	Leu	Thr	Pro	Gly	Leu	Arg	Cys	Leu	Asn
	1300					1305					1310			
ctg gat	gtg tac	agg ata	ctg	ctg ttg	atg gtc	gga	ata ggc	agc						
4080														
Leu	Asp	Val	Tyr	Arg	Ile	Leu	Leu	Leu	Met	Val	Gly	Ile	Gly	Ser
	1315					1320					1325			
ttg atc	agg gag	aag agg	agt	gca gct	gca aaa	aag	aaa gga	gca						
4125														
Leu	Ile	Arg	Glu	Lys	Arg	Ser	Ala	Ala	Ala	Lys	Lys	Lys	Gly	Ala
	1330					1335					1340			
agt ctg	cta tgc	ttg gct	cta	gcc tca	aca gga	ctt	ttc aac	ccc						
4170														
Ser	Leu	Leu	Cys	Leu	Ala	Leu	Ala	Ser	Thr	Gly	Leu	Phe	Asn	Pro
	1345					1350					1355			
atg atc	ctt gct	gct gga	ctg	att gca	tgt gat	ccc	aac cgt	aaa						
4215														
Met	Ile	Leu	Ala	Ala	Gly	Leu	Ile	Ala	Cys	Asp	Pro	Asn	Arg	Lys
	1360					1365					1370			
cgc gga	tgg ccc	gca act	gaa	gtg atg	aca gct	gtc	ggc cta	atg						
4260														
Arg	Gly	Trp	Pro	Ala	Thr	Glu	Val	Met	Thr	Ala	Val	Gly	Leu	Met
	1375					1380					1385			

REPLACEMENT SHEET

Figure 12 continued

ttt gcc	atc gtc	gga ggg	ctg gca	gag ctt	gac att	gac tcc	atg
4305							
Phe Ala	Ile Val	Gly Gly	Leu Ala	Glu Leu	Asp Ile	Asp Ser	Met
1390			1395		1400		
gcc att	cca atg	act atc	gcg ggg	ctc atg	ttt gct	gct ttc	gtg
4350							
Ala Ile	Pro Met	Thr Ile	Ala Gly	Leu Met	Phe Ala	Ala Phe	Val
1405			1410		1415		
att tct	ggg aaa	tca aca	gat atg	tgg att	gag aga	acg gcg	gac
4395							
Ile Ser	Gly Lys	Ser Thr	Asp Met	Trp Ile	Glu Arg	Thr Ala	Asp
1420			1425		1430		
att tcc	tgg gaa	agt gat	gca gaa	att aca	ggc tcg	agc gaa	aga
4440							
Ile Ser	Trp Glu	Ser Asp	Ala Glu	Ile Thr	Gly Ser	Ser Glu	Arg
1435			1440		1445		
gtt gat	gtg cgg	ctt gat	gat gat	gga aac	ttc cag	ctc atg	aat
4485							
Val Asp	Val Arg	Leu Asp	Asp Asp	Gly Asn	Phe Gln	Leu Met	Asn
1450			1455		1460		
gat cca	gga gca	cct tgg	aag ata	tgg atg	ctc aga	atg gtc	tgt
4530							
Asp Pro	Gly Ala	Pro Trp	Lys Ile	Trp Met	Leu Arg	Met Val	Cys
1465			1470		1475		
ctc gcg	att agt	gcg tac	acc ccc	tgg gca	atc ttg	ccc tca	gta
4575							
Leu Ala	Ile Ser	Ala Tyr	Thr Pro	Trp Ala	Ile Leu	Pro Ser	Val
1480			1485		1490		
gtt gga	ttt tgg	ata act	ctc caa	tac aca	aag aga	gga ggc	gtg
4620							
Val Gly	Phe Trp	Ile Thr	Leu Gln	Tyr Thr	Lys Arg	Gly Gly	Val
1495			1500		1505		
ttg tgg	gac act	ccc tca	cca aag	gag tac	aaa aag	ggg gac	acg
4665							
Leu Trp	Asp Thr	Pro Ser	Pro Lys	Glu Tyr	Lys Lys	Gly Asp	Thr
1510			1515		1520		
acc acc	ggc gtc	tac agg	atc atg	act cgt	ggg ctg	ctc ggc	agt
4710							
Thr Thr	Gly Val	Tyr Arg	Ile Met	Thr Arg	Gly Leu	Leu Gly	Ser
1525			1530		1535		

REPLACEMENT SHEET

Figure 12 continued

tat caa	gca gga gcg ggc gtg	atg gtt gaa ggt gtt	ttc cac acc
4755			
Tyr Gln	Ala Gly Ala Gly Val	Met Val Glu Gly Val	Phe His Thr
1540	1545	1550	
ctt tgg	cat aca aca aaa gga	gcc gct ttg atg agc	gga gag ggc
4800			
Leu Trp	His Thr Thr Lys Gly	Ala Ala Leu Met Ser	Gly Glu Gly
1555	1560	1565	
cgc ctg	gac cca tac tgg ggc	agt gtc aag gag gat	cga ctt tgt
4845			
Arg Leu	Asp Pro Tyr Trp Gly	Ser Val Lys Glu Asp	Arg Leu Cys
1570	1575	1580	
tac gga	gga ccc tgg aaa ttg	cag cac aag tgg aac	ggg cag gat
4890			
Tyr Gly	Gly Pro Trp Lys Leu	Gln His Lys Trp Asn	Gly Gln Asp
1585	1590	1595	
gag gtg	cag atg att gtg gtg	gaa cct ggc aag aac	gtt aag aac
4935			
Glu Val	Gln Met Ile Val Val	Glu Pro Gly Lys Asn	Val Lys Asn
1600	1605	1610	
gtc cag	acg aaa cca ggg gtg	ttc aaa aca cct gaa	gga gaa atc
4980			
Val Gln	Thr Lys Pro Gly Val	Phe Lys Thr Pro Glu	Gly Glu Ile
1615	1620	1625	
ggg gcc	gtg act ttg gac ttc	ccc act gga aca tca	ggc tca cca
5025			
Gly Ala	Val Thr Leu Asp Phe	Pro Thr Gly Thr Ser	Gly Ser Pro
1630	1635	1640	
ata gtg	gac aaa aac ggt gat	gtg att ggg ctt tat	ggc aat gga
5070			
Ile Val	Asp Lys Asn Gly Asp	Val Ile Gly Leu Tyr	Gly Asn Gly
1645	1650	1655	
gtc ata	atg ccc aac ggc tca	tac ata agc gcg ata	gtg cag ggt
5115			
Val Ile	Met Pro Asn Gly Ser	Tyr Ile Ser Ala Ile	Val Gln Gly
1660	1665	1670	
gaa agg	atg gat gag cca atc	cca gcc gga ttc gaa	cct gag atg
5160			
Glu Arg	Met Asp Glu Pro Ile	Pro Ala Gly Phe Glu	Pro Glu Met
1675	1680	1685	

REPLACEMENT SHEET

Figure 12 continued

ctg agg	aaa aaa	cag atc	act	gta ctg	gat ctc	cat	ccc ggc	gcc						
5205	Leu Arg	Lys Lys	Gln Ile	Thr	Val Leu	Asp Leu	His	Pro Gly	Ala					
	1690			1695			1700							
ggt aaa	aca agg	agg att	ctg	cca cag	atc atc	aaa	gag gcc	ata						
5250	Gly Lys	Thr Arg	Arg Ile	Leu	Pro Gln	Ile Ile	Lys	Glu Ala	Ile					
	1705			1710			1715							
aac aga	aga ctg	aga aca	gcc	gtg cta	gca cca	acc	agg gtt	gtg						
5295	Asn Arg	Arg Leu	Arg Thr	Ala	Val Leu	Ala Pro	Thr	Arg Val	Val					
	1720			1725			1730							
gct gct	gag atg	gct gaa	gca	ctg aga	gga ctg	ccc	atc cgg	tac						
5340	Ala Ala	Glu Met	Ala Glu	Ala	Leu Arg	Gly Leu	Pro	Ile Arg	Tyr					
	1735			1740			1745							
cag aca	tcc gca	gtg ccc	aga	gaa cat	aat gga	aat	gag att	gtt						
5385	Gln Thr	Ser Ala	Val Pro	Arg	Glu His	Asn Gly	Asn	Glu Ile	Val					
	1750			1755			1760							
gat gtc	atg tgt	cat gct	acc	ctc acc	cac agg	ctg	atg tct	cct						
5430	Asp Val	Met Cys	His Ala	Thr	Leu Thr	His Arg	Leu	Met Ser	Pro					
	1765			1770			1775							
cac agg	gtg ccg	aac tac	aac	ctg ttc	gtg atg	gat	gag gct	cat						
5475	His Arg	Val Pro	Asn Tyr	Asn	Leu Phe	Val Met	Asp	Glu Ala	His					
	1780			1785			1790							
ttc acc	gac cca	gct agc	att	gca gca	aga ggt	tac	att tcc	aca						
5520	Phe Thr	Asp Pro	Ala Ser	Ile	Ala Ala	Arg Gly	Tyr	Ile Ser	Thr					
	1795			1800			1805							
aag gtc	gag cta	ggg gag	gcg	gcg gca	ata ttc	atg	aca gcc	acc						
5565	Lys Val	Glu Leu	Gly Glu	Ala	Ala Ala	Ile Phe	Met	Thr Ala	Thr					
	1810			1815			1820							
cca cca	ggc act	tca gat	cca	ttc cca	gag tcc	aat	tca cca	att						
5610	Pro Pro	Gly Thr	Ser Asp	Pro	Phe Pro	Glu Ser	Asn	Ser Pro	Ile					
	1825			1830			1835							

REPLACEMENT SHEET

Figure 12 continued

tcc gac	tta cag	act gag	atc ccg	gat cga	gct tgg	aac tct	gga	
5655								
Ser Asp	Leu Gln	Thr Glu	Ile	Pro Asp	Arg Ala	Trp	Asn Ser	Gly
1840			1845			1850		
tac gaa	tgg atc	aca gaa	tac acc	ggg aag	acg gtt	tgg ttt	gtg	
5700								
Tyr Glu	Trp Ile	Thr Glu	Tyr	Thr Gly	Lys Thr	Val	Trp Phe	Val
1855			1860			1865		
cct agt	gtc aag	atg ggg	aat gag	att gcc	ctt tgc	cta caa	cgt	
5745								
Pro Ser	Val Lys	Met Gly	Asn	Glu Ile	Ala Leu	Cys	Leu Gln	Arg
1870			1875			1880		
gct gga	aag aaa	gta gtc	caa ttg	aac aga	aag tcg	tac gag	acg	
5790								
Ala Gly	Lys Lys	Val Val	Gln	Leu Asn	Arg Lys	Ser	Tyr Glu	Thr
1885			1890			1895		
gag tac	cca aaa	tgt aag	aac gat	gat gat	tgg gac	ttt gtt	atc aca	
5835								
Glu Tyr	Pro Lys	Cys Lys	Asn	Asp Asp	Trp Asp	Phe	Val Ile	Thr
1900			1905			1910		
aca gac	ata tct	gaa atg	ggg gct	aac ttc	aag gcg	agc agg	gtg	
5880								
Thr Asp	Ile Ser	Glu Met	Gly	Ala Asn	Phe Lys	Ala	Ser Arg	Val
1915			1920			1925		
att gac	agc cgg	aag agt	gtg aaa	cca acc	atc ata	aca gaa	gga	
5925								
Ile Asp	Ser Arg	Lys Ser	Val	Lys Pro	Thr Ile	Ile	Thr Glu	Gly
1930			1935			1940		
gaa ggg	aga gtg	atc ctg	gga gaa	cca tct	gca gtg	aca gca	gct	
5970								
Glu Gly	Arg Val	Ile Leu	Gly	Glu Pro	Ser Ala	Val	Thr Ala	Ala
1945			1950			1955		
agt gcc	gcc cag	aga cgt	gga cgt	atc ggt	aga aat	ccg tcg	caa	
6015								
Ser Ala	Ala Gln	Arg Arg	Gly	Arg Ile	Gly Arg	Asn	Pro Ser	Gln
1960			1965			1970		
gtt ggt	gat gag	tac tgt	tat ggg	ggg cac	acg aat	gaa gac	gac	
6060								
Val Gly	Asp Glu	Tyr Cys	Tyr	Gly Gly	His Thr	Asn	Glu Asp	Asp
1975			1980			1985		

REPLACEMENT SHEET

Figure 12 continued

tcg aac	ttc gcc	cat tgg	act gag	gca cga	atc atg	ctg gac	aac
6105							
Ser Asn	Phe Ala	His Trp	Thr	Glu Ala	Arg Ile	Met	Leu Asp Asn
1990			1995			2000	
atc aac	atg cca	aac gga	ctg atc	gct caa	ttc tac	caa cca	gag
6150							
Ile Asn	Met Pro	Asn Gly	Leu	Ile Ala	Gln Phe	Tyr	Gln Pro Glu
2005			2010			2015	
cgt gag	aag gta	tat acc	atg gat	ggg gaa	tac cgg	ctc aga	gga
6195							
Arg Glu	Lys Val	Tyr Thr	Met	Asp Gly	Glu Tyr	Arg	Leu Arg Gly
2020			2025			2030	
gaa gag	aga aaa	aac ttt	ctg gaa	ctg ttg	agg act	gca gat	ctg
6240							
Glu Glu	Arg Lys	Asn Phe	Leu	Glu Leu	Leu Arg	Thr	Ala Asp Leu
2035			2040			2045	
cca gtt	tgg ctg	gct tac	aag gtt	gca gcg	gct gga	gtg tca	tac
6285							
Pro Val	Trp Leu	Ala Tyr	Lys	Val Ala	Ala Ala	Gly	Val Ser Tyr
2050			2055			2060	
cac gac	cgg agg	tgg tgc	ttt gat	ggt cct	agg aca	aac aca	att
6330							
His Asp	Arg Arg	Trp Cys	Phe	Asp Gly	Pro Arg	Thr	Asn Thr Ile
2065			2070			2075	
tta gaa	gac aac	aac gaa	gtg gaa	gtc atc	acg aag	ctt ggt	gaa
6375							
Leu Glu	Asp Asn	Asn Glu	Val	Glu Val	Ile Thr	Lys	Leu Gly Glu
2080			2085			2090	
agg aag	att ctg	agg ccg	cgc tgg	att gac	gcc agg	gtg tac	tcg
6420							
Arg Lys	Ile Leu	Arg Pro	Arg	Trp Ile	Asp Ala	Arg	Val Tyr Ser
2095			2100			2105	
gat cac	cag gca	cta aag	gcg ttc	aag gac	ttc gcc	tcg gga	aaa
6465							
Asp His	Gln Ala	Leu Lys	Ala	Phe Lys	Asp Phe	Ala	Ser Gly Lys
2110			2115			2120	
cgt tct	cag ata	ggg ctc	att gag	gtt ctg	gga aag	atg cct	gag
6510							
Arg Ser	Gln Ile	Gly Leu	Ile	Glu Val	Leu Gly	Lys	Met Pro Glu
2125			2130			2135	

REPLACEMENT SHEET

Figure 12 continued

cac ttc	atg ggg aag aca tgg	gaa gca ctt gac acc	atg tac gtt
6555			
His Phe	Met Gly Lys Thr	Trp Glu Ala Leu Asp Thr	Met Tyr Val
2140		2145	2150
gtg gcc	act gca gag aaa gga	gga aga gct cac aga	atg gcc ctg
6600			
Val Ala	Thr Ala Glu Lys	Gly Gly Arg Ala His Arg	Met Ala Leu
2155		2160	2165
gag gaa	ctg cca gat gct ctt	cag aca att gcc ttg	att gcc tta
6645			
Glu Glu	Leu Pro Asp Ala	Leu Gln Thr Ile Ala Leu	Ile Ala Leu
2170		2175	2180
ttg agt	gtg atg acc atg gga	gta ttc ttc ctc ctc	atg cag cgg
6690			
Leu Ser	Val Met Thr Met	Gly Val Phe Phe Leu Leu	Met Gln Arg
2185		2190	2195
aag ggc	att gga aag ata ggt	ttg gga ggc gct gtc	ttg gga gtc
6735			
Lys Gly	Ile Gly Lys Ile	Gly Leu Gly Gly Ala Val	Leu Gly Val
2200		2205	2210
gcg acc	ttt ttc tgt tgg atg	gct gaa gtt cca gga	acg aag atc
6780			
Ala Thr	Phe Phe Cys Trp	Met Ala Glu Val Pro Gly	Thr Lys Ile
2215		2220	2225
gcc gga	atg ttg ctg ctc tcc	ctt ctc ttg atg att	gtg cta att
6825			
Ala Gly	Met Leu Leu Leu	Ser Leu Leu Leu Met Ile	Val Leu Ile
2230		2235	2240
cct gag	cca gag aag caa cgt	tcg cag aca gac aac	cag cta gcc
6870			
Pro Glu	Pro Glu Lys Gln	Arg Ser Gln Thr Asp Asn	Gln Leu Ala
2245		2250	2255
gtg ttc	ctg att tgt gtc atg	acc ctt gtg agc gca	gtg gca gcc
6915			
Val Phe	Leu Ile Cys Val	Met Thr Leu Val Ser Ala	Val Ala Ala
2260		2265	2270
aac gag	atg ggt tgg cta gat	aag acc aag agt gac	ata agc agt
6960			
Asn Glu	Met Gly Trp Leu	Asp Lys Thr Lys Ser Asp	Ile Ser Ser
2275		2280	2285

REPLACEMENT SHEET

Figure 12 continued

ttg ttt	ggg caa aga att gag	gtc aag gag aat ttc	agc atg gga
7005			
Leu Phe	Gly Gln Arg Ile Glu	Val Lys Glu Asn Phe	Ser Met Gly
2290	2295	2300	
gag ttt	ctt ttg gac ttg agg	ccg gca aca gcc tgg	tca ctg tac
7050			
Glu Phe	Leu Leu Asp Leu Arg	Pro Ala Thr Ala Trp	Ser Leu Tyr
2305	2310	2315	
gct gtg	aca aca gcg gtc ctc	act cca ctg cta aag	cat ttg atc
7095			
Ala Val	Thr Thr Ala Val Leu	Thr Pro Leu Leu Lys	His Leu Ile
2320	2325	2330	
acg tca	gat tac atc aac acc	tca ttg acc tca ata	aac gtt cag
7140			
Thr Ser	Asp Tyr Ile Asn Thr	Ser Leu Thr Ser Ile	Asn Val Gln
2335	2340	2345	
gca agt	gca cta ttc aca ctc	gcg cga ggc ttc ccc	ttc gtc gat
7185			
Ala Ser	Ala Leu Phe Thr Leu	Ala Arg Gly Phe Pro	Phe Val Asp
2350	2355	2360	
gtt gga	gtg tcg gct ctc ctg	cta gca gcc gga tgc	tgg gga caa
7230			
Val Gly	Val Ser Ala Leu Leu	Leu Ala Ala Gly Cys	Trp Gly Gln
2365	2370	2375	
gtc acc	ctc acc gtt acg gta	aca gcg gca aca ctc	ctt ttt tgc
7275			
Val Thr	Leu Thr Val Thr Val	Thr Ala Ala Thr Leu	Leu Phe Cys
2380	2385	2390	
cac tat	gcc tac atg gtt ccc	ggt tgg caa gct gag	gca atg cgc
7320			
His Tyr	Ala Tyr Met Val Pro	Gly Trp Gln Ala Glu	Ala Met Arg
2395	2400	2405	
tca gcc	cag cgg cgg aca gcg	gcc gga atc atg aag	aac gct gta
7365			
Ser Ala	Gln Arg Arg Thr Ala	Ala Gly Ile Met Lys	Asn Ala Val
2410	2415	2420	
gtg gat	ggc atc gtg gcc acg	gac gtc cca gaa tta	gag cgc acc
7410			
Val Asp	Gly Ile Val Ala Thr	Asp Val Pro Glu Leu	Glu Arg Thr
2425	2430	2435	

REPLACEMENT SHEET

Figure 12 continued

aca 7455	ccc	atc	atg	cag	aag	aaa	gtt	gga	cag	atc	atg	ctg	atc	ttg
Thr	Pro 2440	Ile	Met	Gln	Lys	Lys 2445	Val	Gly	Gln	Ile	Met 2450	Leu	Ile	Leu
gtg 7500	tct	cta	gct	gca	gta	gta	gtg	aac	ccg	tct	gtg	aag	aca	gta
Val	Ser 2455	Leu	Ala	Ala	Val	Val 2460	Val	Asn	Pro	Ser	Val 2465	Lys	Thr	Val
cga 7545	gaa	gcc	gga	att	ttg	atc	acg	gcc	gca	gcg	gtg	acg	ctt	tgg
Arg	Glu 2470	Ala	Gly	Ile	Leu	Ile 2475	Thr	Ala	Ala	Ala	Val 2480	Thr	Leu	Trp
gag 7590	aat	gga	gca	agc	tct	gtt	tgg	aac	gca	aca	act	gcc	atc	gga
Glu	Asn 2485	Gly	Ala	Ser	Ser	Val 2490	Trp	Asn	Ala	Thr	Thr 2495	Ala	Ile	Gly
ctc 7635	tgc	cac	atc	atg	cgt	ggg	ggg	tgg	ttg	tca	tgt	cta	tcc	ata
Leu	Cys 2500	His	Ile	Met	Arg	Gly 2505	Gly	Trp	Leu	Ser	Cys 2510	Leu	Ser	Ile
aca 7680	tgg	aca	ctc	ata	aag	aac	atg	gaa	aaa	cca	gga	cta	aaa	aga
Thr	Trp 2515	Thr	Leu	Ile	Lys	Asn 2520	Met	Glu	Lys	Pro	Gly 2525	Leu	Lys	Arg
ggg 7725	ggg	gca	aaa	gga	cgc	acc	ttg	gga	gag	gtt	tgg	aaa	gaa	aga
Gly	Gly 2530	Ala	Lys	Gly	Arg	Thr 2535	Leu	Gly	Glu	Val	Trp 2540	Lys	Glu	Arg
ctc 7770	aac	cag	atg	aca	aaa	gaa	gag	ttc	act	agg	tac	cgc	aaa	gag
Leu	Asn 2545	Gln	Met	Thr	Lys	Glu 2550	Glu	Phe	Thr	Arg	Tyr 2555	Arg	Lys	Glu
gcc 7815	atc	atc	gaa	gtc	gat	cgc	tca	gcg	gca	aaa	cac	gcc	agg	aaa
Ala	Ile 2560	Ile	Glu	Val	Asp	Arg 2565	Ser	Ala	Ala	Lys	His 2570	Ala	Arg	Lys
gaa 7860	ggc	aat	gtc	act	gga	ggg	cat	cca	gtc	tct	agg	ggc	aca	gca
Glu	Gly 2575	Asn	Val	Thr	Gly	Gly 2580	His	Pro	Val	Ser	Arg 2585	Gly	Thr	Ala

REPLACEMENT SHEET

Figure 12 continued

aaa	ctg	aga	tgg	ctg	gtc	gaa	cgg	agg	ttt	ctc	gaa	cgg	gtc	gga	
7905	Lys	Leu	Arg	Trp	Leu	Val	Glu	Arg	Arg	Phe	Leu	Glu	Pro	Val	Gly
	2590						2595					2600			
aaa	gtg	att	gac	ctt	gga	tgt	gga	aga	ggc	ggt	tgg	tgt	tac	tat	
7950	Lys	Val	Ile	Asp	Leu	Gly	Cys	Gly	Arg	Gly	Gly	Trp	Cys	Tyr	Tyr
	2605						2610					2615			
atg	gca	acc	caa	aaa	aga	gtc	caa	gaa	gtc	aga	ggg	tac	aca	aag	
7995	Met	Ala	Thr	Gln	Lys	Arg	Val	Gln	Glu	Val	Arg	Gly	Tyr	Thr	Lys
	2620						2625					2630			
ggc	ggt	ccc	gga	cat	gaa	gag	ccc	caa	cta	gtg	caa	agt	tat	gga	
8040	Gly	Gly	Pro	Gly	His	Glu	Glu	Pro	Gln	Leu	Val	Gln	Ser	Tyr	Gly
	2635						2640					2645			
tgg	aac	att	gtc	acc	atg	aag	agt	gga	gtg	gat	gtg	ttc	tac	aga	
8085	Trp	Asn	Ile	Val	Thr	Met	Lys	Ser	Gly	Val	Asp	Val	Phe	Tyr	Arg
	2650						2655					2660			
cct	tct	gag	tgt	tgt	gac	acc	ctc	ctt	tgt	gac	atc	gga	gag	tcc	
8130	Pro	Ser	Glu	Cys	Cys	Asp	Thr	Leu	Leu	Cys	Asp	Ile	Gly	Glu	Ser
	2665						2670					2675			
tcg	tca	agt	gct	gag	gtt	gaa	gag	cat	agg	acg	att	cgg	gtc	ctt	
8175	Ser	Ser	Ser	Ala	Glu	Val	Glu	Glu	His	Arg	Thr	Ile	Arg	Val	Leu
	2680						2685					2690			
gaa	atg	gtt	gag	gac	tgg	ctg	cac	cga	ggg	cca	agg	gaa	ttt	tgc	
8220	Glu	Met	Val	Glu	Asp	Trp	Leu	His	Arg	Gly	Pro	Arg	Glu	Phe	Cys
	2695						2700					2705			
gtg	aag	gtg	ctc	tgc	ccc	tac	atg	ccg	aaa	gtc	ata	gag	aag	atg	
8265	Val	Lys	Val	Leu	Cys	Pro	Tyr	Met	Pro	Lys	Val	Ile	Glu	Lys	Met
	2710						2715					2720			
gag	ctg	ctc	caa	cgc	cgg	tat	ggg	ggg	gga	ctg	gtc	aga	aac	cca	
8310	Glu	Leu	Leu	Gln	Arg	Arg	Tyr	Gly	Gly	Gly	Leu	Val	Arg	Asn	Pro
	2725						2730					2735			

REPLACEMENT SHEET

Figure 12 continued

ctc tca	cgg aat tcc acg cac	gag atg tat tgg gtg	agt cga gct
8355			
Leu Ser	Arg Asn Ser Thr His	Glu Met Tyr Trp Val	Ser Arg Ala
2740	2745	2750	
tca ggc	aat gtg gta cat tca	gtg aat atg acc agc	cag gtg ctc
8400			
Ser Gly	Asn Val Val His Ser	Val Asn Met Thr Ser	Gln Val Leu
2755	2760	2765	
cta gga	aga atg gaa aaa agg	acc tgg aag gga ccc	caa tac gag
8445			
Leu Gly	Arg Met Glu Lys Arg	Thr Trp Lys Gly Pro	Gln Tyr Glu
2770	2775	2780	
gaa gat	gta aac ttg gga agt	gga acc agg gcg gtg	gga aaa ccc
8490			
Glu Asp	Val Asn Leu Gly Ser	Gly Thr Arg Ala Val	Gly Lys Pro
2785	2790	2795	
ctg ctc	aac tca gac acc agt	aaa atc aag aac agg	att gaa cga
8535			
Leu Leu	Asn Ser Asp Thr Ser	Lys Ile Lys Asn Arg	Ile Glu Arg
2800	2805	2810	
ctc agg	cgt gag tac agt tcg	acg tgg cac cac gat	gag aac cac
8580			
Leu Arg	Arg Glu Tyr Ser Ser	Thr Trp His His Asp	Glu Asn His
2815	2820	2825	
cca tat	aga acc tgg aac tat	cac ggc agt tat gat	gtg aag ccc
8625			
Pro Tyr	Arg Thr Trp Asn Tyr	His Gly Ser Tyr Asp	Val Lys Pro
2830	2835	2840	
aca ggc	tcc gcc agt tcg ctg	gtc aat gga gtg gtc	agg ctc ctc
8670			
Thr Gly	Ser Ala Ser Ser Leu	Val Asn Gly Val Val	Arg Leu Leu
2845	2850	2855	
tca aaa	cca tgg gac acc atc	acg aat gtt acc acc	atg gcc atg
8715			
Ser Lys	Pro Trp Asp Thr Ile	Thr Asn Val Thr Thr	Met Ala Met
2860	2865	2870	
act gac	act act ccc ttc ggg	cag cag cga gtg ttc	aaa gag aag
8760			
Thr Asp	Thr Thr Pro Phe Gly	Gln Gln Arg Val Phe	Lys Glu Lys
2875	2880	2885	

REPLACEMENT SHEET

Figure 12 continued

gtg gac	acg aaa gct cct gaa	ccg cca gaa gga gtg	aag tac gtg
8805			
Val Asp	Thr Lys Ala Pro Glu	Pro Pro Glu Gly Val	Lys Tyr Val
2890	2895	2900	
ctc aat	gag acc acc aac tgg	ttg tgg gcg ttt ttg	gcc aga gaa
8850			
Leu Asn	Glu Thr Thr Asn Trp	Leu Trp Ala Phe Leu	Ala Arg Glu
2905	2910	2915	
aaa cgt	ccc aga atg tgc tct	cga gag gaa ttc ata	aga aag gtc
8895			
Lys Arg	Pro Arg Met Cys Ser	Arg Glu Glu Phe Ile	Arg Lys Val
2920	2925	2930	
aac agc	aat gca gct ttg ggt	gcc atg ttt gaa gag	cag aat caa
8940			
Asn Ser	Asn Ala Ala Leu Gly	Ala Met Phe Glu Glu	Gln Asn Gln
2935	2940	2945	
tgg agg	agc gcc aga gaa gca	gtt gaa gat cca aaa	ttt tgg gag
8985			
Trp Arg	Ser Ala Arg Glu Ala	Val Glu Asp Pro Lys	Phe Trp Glu
2950	2955	2960	
atg gtg	gat gag gag cgc gag	gca cat ctg cgg ggg	gaa tgt cac
9030			
Met Val	Asp Glu Glu Arg Glu	Ala His Leu Arg Gly	Glu Cys His
2965	2970	2975	
act tgc	att tac aac atg atg	gga aag aga gag aaa	aaa ccc gga
9075			
Thr Cys	Ile Tyr Asn Met Met	Gly Lys Arg Glu Lys	Lys Pro Gly
2980	2985	2990	
gag ttc	gga aag gcc aag gga	agc aga gcc att tgg	ttc atg tgg
9120			
Glu Phe	Gly Lys Ala Lys Gly	Ser Arg Ala Ile Trp	Phe Met Trp
2995	3000	3005	
ctc gga	gct cgc ttt ctg gag	ttc gag gct ctg ggt	ttt ctc aat
9165			
Leu Gly	Ala Arg Phe Leu Glu	Phe Glu Ala Leu Gly	Phe Leu Asn
3010	3015	3020	
gaa gac	cac tgg ctt gga aga	aag aac tca gga gga	ggg gtc gag
9210			
Glu Asp	His Trp Leu Gly Arg	Lys Asn Ser Gly Gly	Gly Val Glu
3025	3030	3035	

REPLACEMENT SHEET

Figure 12 continued

ggc	ttg	ggc	ctc	caa	aaa	ctg	ggg	tac	atc	ctg	cgt	gaa	gtt	ggc
9255														
Gly	Leu	Gly	Leu	Gln	Lys	Leu	Gly	Tyr	Ile	Leu	Arg	Glu	Val	Gly
	3040					3045					3050			
acc	cgg	cct	ggg	ggc	aag	atc	tat	gct	gat	gac	aca	gct	ggc	tgg
9300														
Thr	Arg	Pro	Gly	Gly	Lys	Ile	Tyr	Ala	Asp	Asp	Thr	Ala	Gly	Trp
	3055					3060					3065			
gac	acc	cgc	atc	acg	aga	gct	gac	ttg	gaa	aat	gaa	gct	aag	gtg
9345														
Asp	Thr	Arg	Ile	Thr	Arg	Ala	Asp	Leu	Glu	Asn	Glu	Ala	Lys	Val
	3070					3075					3080			
ctt	gag	ctg	ctt	gat	ggg	gaa	cat	cgg	cgt	ctt	gcc	agg	gcc	atc
9390														
Leu	Glu	Leu	Leu	Asp	Gly	Glu	His	Arg	Arg	Leu	Ala	Arg	Ala	Ile
	3085					3090					3095			
att	gag	ctc	acc	tat	cgt	cac	aaa	gtt	gtg	aaa	gtg	atg	cgc	ccg
9435														
Ile	Glu	Leu	Thr	Tyr	Arg	His	Lys	Val	Val	Lys	Val	Met	Arg	Pro
	3100					3105					3110			
gct	gct	gat	gga	aga	acc	gtc	atg	gat	gtt	atc	tcc	aga	gaa	gat
9480														
Ala	Ala	Asp	Gly	Arg	Thr	Val	Met	Asp	Val	Ile	Ser	Arg	Glu	Asp
	3115					3120					3125			
cag	agg	ggg	agt	gga	caa	gtt	gtc	acc	tac	gcc	cta	aac	act	ttc
9525														
Gln	Arg	Gly	Ser	Gly	Gln	Val	Val	Thr	Tyr	Ala	Leu	Asn	Thr	Phe
	3130					3135					3140			
acc	aac	ctg	gcc	gtc	cag	ctg	gtg	agg	atg	atg	gaa	ggg	gaa	gga
9570														
Thr	Asn	Leu	Ala	Val	Gln	Leu	Val	Arg	Met	Met	Glu	Gly	Glu	Gly
	3145					3150					3155			
gtg	att	ggc	cca	gat	gat	gtg	gag	aaa	ctc	aca	aaa	ggg	aaa	gga
9615														
Val	Ile	Gly	Pro	Asp	Asp	Val	Glu	Lys	Leu	Thr	Lys	Gly	Lys	Gly
	3160					3165					3170			
ccc	aaa	gtc	agg	acc	tgg	ctg	ttt	gag	aat	ggg	gaa	gaa	aga	ctc
9660														
Pro	Lys	Val	Arg	Thr	Trp	Leu	Phe	Glu	Asn	Gly	Glu	Glu	Arg	Leu
	3175					3180					3185			

REPLACEMENT SHEET

Figure 12 continued

agc cgc	atg gct gtc agt gga	gat gac tgt gtg gta	aag ccc ctg
9705			
Ser Arg	Met Ala Val Ser Gly	Asp Asp Cys Val Val	Lys Pro Leu
3190	3195	3200	
gac gat	cgc ttt gcc acc tcg	ctc cac ttc ctc aat	gct atg tca
9750			
Asp Asp	Arg Phe Ala Thr Ser	Leu His Phe Leu Asn	Ala Met Ser
3205	3210	3215	
aag gtt	cgc aaa gac atc caa	gag tgg aaa ccg tca	act gga tgg
9795			
Lys Val	Arg Lys Asp Ile Gln	Glu Trp Lys Pro Ser	Thr Gly Trp
3220	3225	3230	
tat gat	tgg cag cag gtt cca	ttt tgc tca aac cat	ttc act gaa
9840			
Tyr Asp	Trp Gln Gln Val Pro	Phe Cys Ser Asn His	Phe Thr Glu
3235	3240	3245	
ttg atc	atg aaa gat gga aga	aca ctg gtg gtt cca	tgc cga gga
9885			
Leu Ile	Met Lys Asp Gly Arg	Thr Leu Val Val Pro	Cys Arg Gly
3250	3255	3260	
cag gat	gaa ttg gta ggc aga	gct cgc ata tct cca	ggg gcc gga
9930			
Gln Asp	Glu Leu Val Gly Arg	Ala Arg Ile Ser Pro	Gly Ala Gly
3265	3270	3275	
tgg aac	gtc cgc gac act gct	tgt ctg gct aag tct	tat gcc cag
9975			
Trp Asn	Val Arg Asp Thr Ala	Cys Leu Ala Lys Ser	Tyr Ala Gln
3280	3285	3290	
atg tgg	ctg ctt ctg tac ttc	cac aga aga gac ctg	cgg ctc atg
10020			
Met Trp	Leu Leu Leu Tyr Phe	His Arg Arg Asp Leu	Arg Leu Met
3295	3300	3305	
gcc aac	gcc att tgc tcc gct	gtc cct gtg aat tgg	gtc cct acc
10065			
Ala Asn	Ala Ile Cys Ser Ala	Val Pro Val Asn Trp	Val Pro Thr
3310	3315	3320	
gga aga	acc acg tgg tcc atc	cat gca gga gga gag	tgg atg aca
10110			
Gly Arg	Thr Thr Trp Ser Ile	His Ala Gly Gly Glu	Trp Met Thr
3325	3330	3335	

REPLACEMENT SHEET

Figure 12 continued

aca gag gac atg ttg gag gtc tgg aac cgt gtt tgg ata gag gag
10155
Thr Glu Asp Met Leu Glu Val Trp Asn Arg Val Trp Ile Glu Glu
3340 3345 3350

aat gaa tgg atg gaa gac aaa acc cca gtg gag aaa tgg agt gac
10200
Asn Glu Trp Met Glu Asp Lys Thr Pro Val Glu Lys Trp Ser Asp
3355 3360 3365

gtc cca tat tca gga aaa cga gag gac atc tgg tgt ggc agc ctg
10245
Val Pro Tyr Ser Gly Lys Arg Glu Asp Ile Trp Cys Gly Ser Leu
3370 3375 3380

att ggc aca aga gcc cga gcc acg tgg gca gaa aac atc cag gtg
10290
Ile Gly Thr Arg Ala Arg Ala Thr Trp Ala Glu Asn Ile Gln Val
3385 3390 3395

gct atc aac caa gtc aga gca atc atc gga gat gag aag tat gtg
10335
Ala Ile Asn Gln Val Arg Ala Ile Ile Gly Asp Glu Lys Tyr Val
3400 3405 3410

gat tac atg agt tca cta aag aga tat gaa gac aca act ttg gtt
10380
Asp Tyr Met Ser Ser Leu Lys Arg Tyr Glu Asp Thr Thr Leu Val
3415 3420 3425

gag gac aca gta ctg tag atatttaatc aattgtaaat agacaatata
10428
Glu Asp Thr Val Leu
3430

agtatgcata aaagtgtagt tttatagtag tatttagtgg tgtagtgta aatagttaag
10488

aaaattttga ggagaaagtc aggccgggaa gttcccgcca ccggaagttg agtagacggt
10548

gctgcctgcg actcaacccc aggaggactg ggtgaacaaa gccgcgaagt gatccatgta
10608

agccctcaga accgtctcgg aaggaggacc ccacatgttg taacttcaaa gcccaatgtc
10668

agaccacgct acggcgtgct actctgcgga gaggcagtc tgcgatagtg cccagaggag
10728

REPLACEMENT SHEET

Figure 12 continued

actgggttaa caaaggcaaa ccaacgcccc acgcggccct agccccggta atggtgttaa
10788

ccagggcgaa aggactagag gttagaggag accccgcggt ttaaagtgca cggcccagcc
10848

tgactgaagc tgtaggtcag gggaaggact agaggttagt ggagaccccg tgccacaaaa
10908

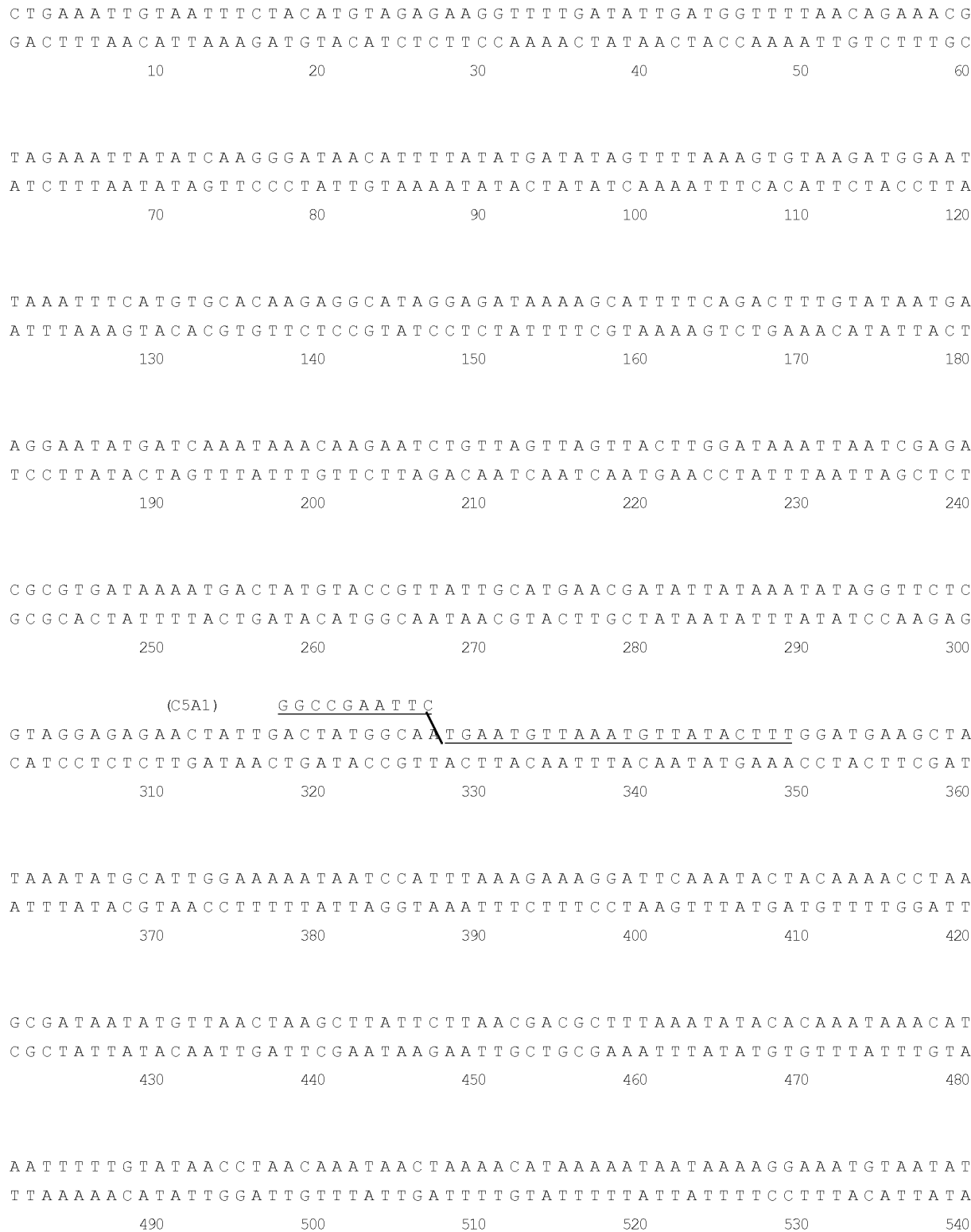
caccacaaca aaacagcata ttgacacctg ggatagacta ggagatcttc tgctctgcac
10968

aaccagccac acggcacagt gcgccgacaa tggcggctgg tggcgcgaga acacaggatc
11028

t
11029

REPLACEMENT SHEET

Figure 13 5kb C5 locus and PCR primers to amplify C5 arms (SEQ ID NO: 77)



REPLACEMENT SHEET

Figure 13 continued

CGTAATTATTTTACTCAGGAATGGGGTTAAATATTTATATCACGTGTATATCTATACTGT
GCATTAATAAAATGAGTCCTTACCCCAATTTATAAATATAGTGACATATAGATATGACA
550 560 570 580 590 600

TATCGTATACTCTTTACAATTACTATTACGAATATGCAAGAGATAATAAGATTACGTATT
ATAGCATATGAGAAATGTTAATGATAAATGCTTATACGTTCTCTATTATTCTAATGCATAA
610 620 630 640 650 660

TAAGAGAATCTTGTCATGATAAATTGGGTACGACATAGTGATAAATGCTATTTTCGCATCGT
ATTCCTCTTAGAACAGTACTATTAACCCATGCTGTATCACTATTTACGATAAAGCGTAGCA
670 680 690 700 710 720

TACATAAAGTCAGTTGGAAAGATGGATTTGACAGATGTAACCTAATAGGTGCAAAAATGT
ATGTATTTTCAGTCAACCTTTCTACCTAAACTGTCTACATTGAATTATCCACGTTTTTACA
730 740 750 760 770 780

TAAATAACAGCATTTCTATCGGAAGATAGGATACCAGTTATATTATACAAAAATCACTGGT
ATTTATTGTGCGTAAGATAGCCTTCTATCCTATGGTCAATATAAATATGTTTTTAGTGACCA
790 800 810 820 830 840

TGGATAAAACAGATTCTGCAATATTCGTAAAAGATGAAGATTACTGCGAATTTGTAAACT
ACCTATTTTGTCTAAGACGTTATAAGCATTTTCTACTTCTAATGACGCTTAAACATTTGA
850 860 870 880 890 900

ATGACAATAAAAAGCCATTTATCTCAACGACATCGTGTAATTCTTCCATGTTTTATGTAT
TACTGTTATTTTTTCGGTAAATAGAGTTGCTGTAGCACATTAAAGAAGGTACAAAATACATA
910 920 930 940 950 960

GTGTTTCAGATATTATGAGATTACTATAAACTTTTTGTATACTTATATTCCGTAAACTAT
CACAAAGTCTATAAATACTCTAATGATATTTGAAAAACATATGAATATAAGGCATTTGATA
970 980 990 1000 1010 1020

ATTAATCATGAAGAAAATGAAAAAGTATAGAAGCTGTTTCACGAGCGGTTGTTGAAAACAA
TAATTAGTACTTCTTTTACTTTTTCATATCTTCGACAAGTGCTCGCCAACAACCTTTTGT
1030 1040 1050 1060 1070 1080

CAAAATTATACATTCAAGATGGCTTACATATACGTCTGTGAGGCTATCATGGATAAATGAC

REPLACEMENT SHEET

Figure 13 continued

G T T T T A A T A T G T A A G T T C T A C C G A A T G T A T A T G C A G A C A C T C C G A T A G T A C C T A T T A C T G
1090 1100 1110 1120 1130 1140
A A T G C A T C T C T A A A T A G G T T T T T G G A C A A T G G A T T C G A C C C T A A C A C G G A A T A T G G T A C T
T T A C G T A G A G A T T T A T C C A A A A A C C T G T T A C C T A A G C T G G G A T T G T G C C T T A T A C C A T G A
1150 1160 1170 1180 1190 1200

C T A C A A T C T C C T C T T G A A A T G G C T G T A A T G T T C A A G A A T A C C G A G G C T A T A A A A A T C T T G
G A T G T T A G A G G A G A A C T T T A C C G A C A T T A C A A G T T C T T A T G G C T C C G A T A T T T T T A G A A C
1210 1220 1230 1240 1250 1260

A T G A G G T A T G G A G C T A A A C C T G T A G T T A C T G A A T G C A C A A C T T C T T G T C T G C A T G A T G C G
T A C T C C A T A C C T C G A T T T T G G A C A T C A A T G A C T T A C G T G T T G A A G A A C A G A C G T A C T A C G C
1270 1280 1290 1300 1310 1320

G T G T T G A G A G A C G A C T A C A A A A T A G T G A A A G A T C T G T T G A A G A A T A A C T A T G T A A A C A A T
C A C A A C T C T C T G C T G A T G T T T T A T C A C T T T C T A G A C A A C T T C T T A T T G A T A C A T T T G T T A
1330 1340 1350 1360 1370 1380

G T T C T T T A C A G C G G A G G C T T T A C T C C T T T G T G T T T G G C A G C T T A C C T T A A C A A A G T T A A T
C A A G A A A T G T C G C C T C C G A A A T G A G G A A A C A C A A A C C G T C G A A T G G A A T T G T T T C A A T T A
1390 1400 1410 1420 1430 1440

T T G G T T A A A C T T C T A T T G G C T C A T T C G G C G G A T G T A G A T A T T T C A A A C A C G G A T C G G T T A
A A C C A A T T T T G A A G A T A A C C G A G T A A G C C G C C T A C A T C T A T A A A G T T T G T G C C T A G C C A A T
1450 1460 1470 1480 1490 1500

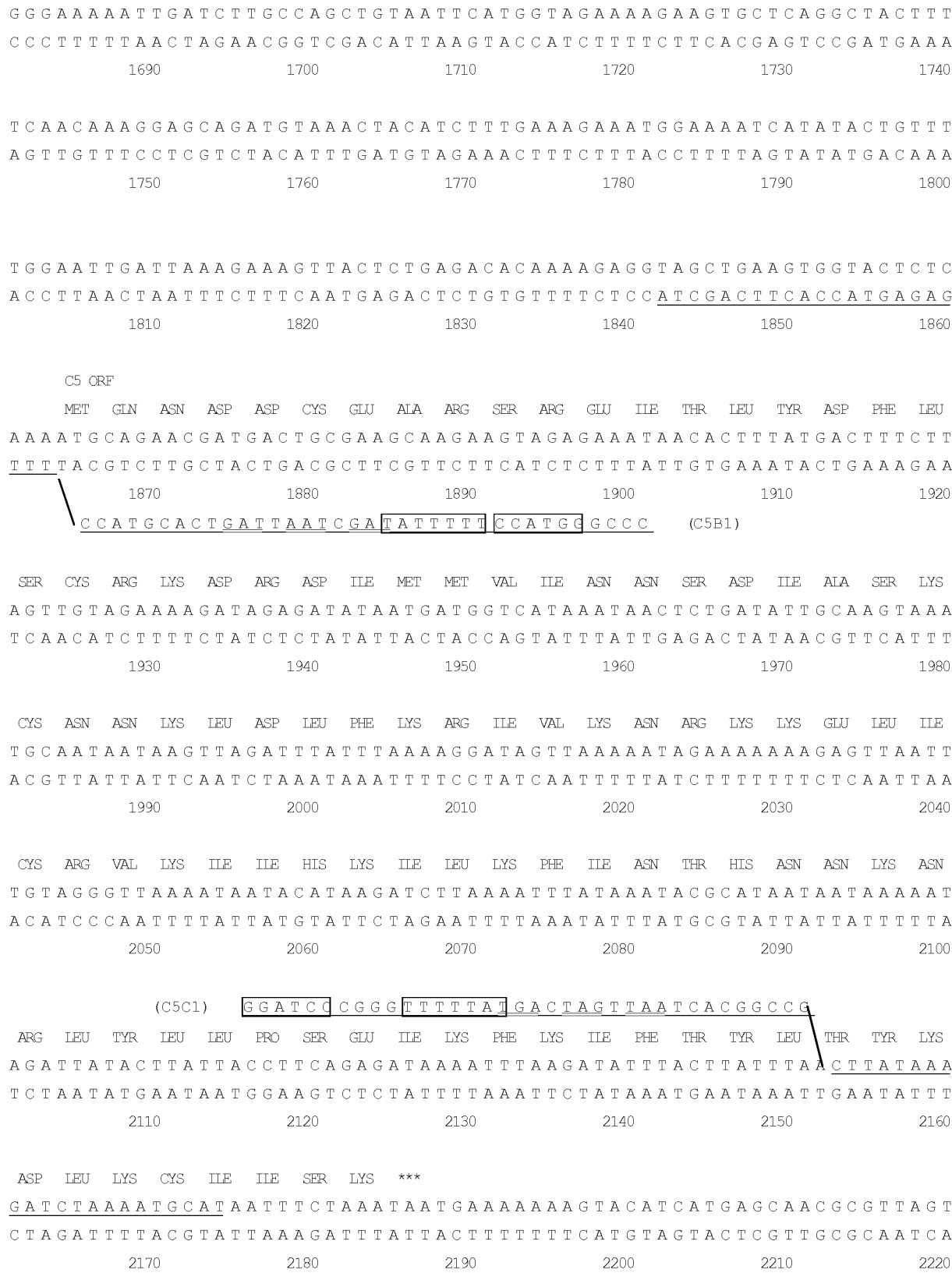
A C T C C T C T A C A T A T A G C C G T A T C A A A T A A A A A T T T A A C A A T G G T T A A A C T T C T A T T G A A C
T G A G G A G A T G T A T A T C G G C A T A G T T T A T T T T T A A A T T G T T A C C A A T T T G A A G A T A A C T T G
1510 1520 1530 1540 1550 1560

A A A G G T G C T G A T A C T G A C T T G C T G G A T A A C A T G G G A C G T A C T C C T T T A A T G A T C G C T G T A
T T T C C A C G A C T A T G A C T G A A C G A C C T A T T G T A C C C T G C A T G A G G A A A T T A C T A G C G A C A T
1570 1580 1590 1600 1610 1620

C A A T C T G G A A A T A T T G A A A T A T G T A G C A C A C T A C T T A A A A A A A T A A A A T G T C C A G A A C T
G T T A G A C C T T T A T A A C T T T A T A C A T C G T G T G A T G A A T T T T T T T A T T T T A C A G G T C T T G A
1630 1640 1650 1660 1670 1680

REPLACEMENT SHEET

Figure 13 continued



REPLACEMENT SHEET

Figure 13 continued

ATATTTTACAAATGGAGATTAAACGCTCTATACCGTTCTATGTTTATTGATTCAGATGATGT
TATAAAATGTTACCTCTAATTGCGAGATATGGCAAGATACAAATAACTAAGTCTACTACA
2230 2240 2250 2260 2270 2280
TTTAGAAAAGAAAGTTATTGAATATGAAAACTTTAAATGAAGATGAAGATGACGACGATGA
AAATCTTTTCTTTCAATAACTTATACTTTTGAAATTACTTCTACTTCTACTGCTGCTACT
2290 2300 2310 2320 2330 2340

TTATTGTTGTAAATCTGTTTTAGATGAAGAAGATGACGCGCTAAAGTATACTATGGTTAC
AATAACAACATTTAGACAAAATCTACTTCTTCTACTGCGCGATTTTCATATGATACCAATG
2350 2360 2370 2380 2390 2400

AAAGTATAAGTCTATACTACTAATGGCGACTTGTGCAAGAAGGTATAGTATAGTGAAAAAT
TTTCATATTCAGATATGATGATTACCGCTGAACACGTTCTTCCATATCATATCACTTTTAA
2410 2420 2430 2440 2450 2460

GTTGTTAGATTATGATTATGAAAAACCAAATAAATCAGATCCATATCTAAAGGTATCTCC
CAACAATCTAATACTAATACTTTTTTGGTTTTATTTAGTCTAGGTATAGATTTCCATAGAGG
2470 2480 2490 2500 2510 2520

TTTGACACATAAATTTTCATCTATTCCTAGTTTTAGAATACTTTTTCATTATATTTGTTTACAGC
AAACGTGTATTAAAGTAGATAAAGGATCAAATCTTATGAAAAGTAATATAAACAAATGTCTG
2530 2540 2550 2560 2570 2580
GACGTCGG (C5D1)

TGAAGACGAAAAAAATATATCGATAAATAGAAGATTATGTTAACTCTGCTAATAAGATGAA
ACTTCTGCTTTTTTTTATATAGCTATTATCTTCTAATAACAATTGAGACGATTATTTCTACTT
2590 2600 2610 2620 2630 2640

ATTGAATGAGTCTGTGATAAATAGCTATAATCAGAGAAGTTCTAAAAGGAAATAAAAAATCT
TAACCTTACTCAGACACTATTATCGATATTAGTCTCTTCAAGATTTTCCTTTATTTTTAGA
2650 2660 2670 2680 2690 2700

AACTGATCAGGATATAAAAAACATTGGCTGATGAAATCAACAAGGAGGAACTGAATATAGC
TTGACTAGTCCTATATTTTTTGTAAACCGACTACTTTAGTTGTTTCCTCCTTGACTTATATCG
2710 2720 2730 2740 2750 2760

TAAACTATTGTTAGATAGAGGGGCCAAAGTAAATTACAAGGATGTTTACGGTTCTTTCAGC
ATTTGATAACAATCTATCTCCCCGGTTTTCATTTAATGTTTCCTACAAATGCCAAGAAGTCG
2770 2780 2790 2800 2810 2820

REPLACEMENT SHEET

Figure 13 continued

TCTCCATAGAGCTGCTATTGGTAGGAAACAGGATATGATAAAGCTGTTAATCGATCATGG
AGAGGTATCTCGACGATAAACCATCCTTTGTCTATACTATTTTCGACAATTAGCTAGTACC
2830 2840 2850 2860 2870 2880
AGCTGATGTAAACTCTTTAACTATTGCTAAAGATAATCTTATTAAAAAAAAAATAATATCA
TCGACTACATTTGAGAAAATTGATAACGATTTCTATTAGAATAATTTTTTTTTTTATTATAGT
2890 2900 2910 2920 2930 2940

CGTTTAGTAATATTAAAAATATATTAAATAACTCTATTACTAATAAACCAGTGGATATGAA
GCAAATCATTATAAATTTTATATAATTATTGAGATAATGATTATTGAGGTCACCTATACTT
2950 2960 2970 2980 2990 3000

CATAATACGAAGTTTATACATTCTCATCAAAATCTTATTGACATCAAGTTAGATTGTGAA
GTATTATGCTTCAAATATGTAAGAGTAGTTTTTAGAATAACTGTAGTTCAATCTAACACTT
3010 3020 3030 3040 3050 3060

AATGAGATTATGAAATTAAGGAATACAAAAATAGGATGTAAGAACTTACTAGAATGTTTT
TTACTCTAATACTTTAATTCCTTATGTTTTTATCCTACATTCTTGAATGATCTTACAAAA
3070 3080 3090 3100 3110 3120

ATCAATAATGATATGAATACAGTATCTAGGGCTATAAAACAATGAAACGATTAAAAATTAT
TAGTTATTACTATACTTATGTCATAGATCCCGATATTTGTTACTTTGCTAATTTTTTAATA
3130 3140 3150 3160 3170 3180

AAAAATCATTTCCCTATATATAATACGCTCATAGAAAAATTCAATTTCTGAAAGTATACTA
TTTTTTAGTAAAGGGATATATATTATGCGAGTATCTTTTTTAAGTAAAGACTTTTCATATGAT
3190 3200 3210 3220 3230 3240

AGACACGAATTATTGGATGGAGTTATAAATTCTTTTCAAGGATTCAATAATAAATTGCCT
TCTGTGCTTAATAACCTACCTCAATATTTAAGAAAAGTTCCTAAGTTATTATTTAACGGA
3250 3260 3270 3280 3290 3300

TACGAGATTCAGTACATTATACTGGAGAATCTTAATAACCATGAACTAAAAAAAAATTTTA
ATGCTCTAAGTCATGTAATATGACCTCTTAGAATTATTGGTACTTGATTTTTTTTTTAAAT
3310 3320 3330 3340 3350 3360

GATAATATACATTTAAAAAGGTAAATAGATCATCTGTTATTATAAGCAAAGATGCTTGTTG
CTATTATATGTAATTTTTTCCATTTATCTAGTAGACAATAATATTCGTTTTCTACGAACAAC
3370 3380 3390 3400 3410 3420

REPLACEMENT SHEET

Figure 13 continued

CCAATAATATACAAACAGGTATTTGTTTTTATTTTTTAACTACATATTTGATGTTTCATTCTC
GGTTATTATATGTTGTCCATAAACAAAAATAAAAATTGATGTATAAACTACAAGTAAGAG
3430 3440 3450 3460 3470 3480
TTTATATAGTATACACAGAAAAATTCATAATCCACTTAGAATTTCTAGTTATCTAGTTTTT
AAATATATCATATGTGTCTTTTAAGTATTAGGTGAATCTTAAAGATCAATAGATCAAAAA
3490 3500 3510 3520 3530 3540

CTAGAATATTGTACTTTATTTCTAATGGAATGGCTCTCCAGCCTAGTAATTTATTAATGT
GATCTTATAACATGAAATAAAGATTACCTTACCGAGAGGTTCGGATCATTAAATAATTACA
3550 3560 3570 3580 3590 3600

TAGCTGATATCTTGAAATCAGGATATTCTGCTCCGTGAAGAGAAAGTCCTCCAAAGTTGT
ATCGACTATAGAACTTTAGTCCTATAAGACGAGGCACCTTCTCTTTTCAGGAGGTTTCAACA
3610 3620 3630 3640 3650 3660

ATATTTCCATCACTTTTCATGGCTTCCTCTTTCCATAGTGTCCTTCTATAAGCTGTCTATAT
TATAAAGGTAGTGAAAGTACCGAAGGAGAAAGGTATCACAGAAGATATTGACAGATATA
3670 3680 3690 3700 3710 3720

ATTGTAAACTTTTTCTGGTTTTATGCATTTTAAACATTTAGCAATCTCATTTTTTCATCACAA
TAACATTTGAAAAGACCAAAATACGTAAAAATTTGTAAATCGTTAGAGTAAAAGTAGTGTT
3730 3740 3750 3760 3770 3780

TTAAGGCACAAATCTAACATGGAATGTCTACCATAACCCAATAAGGTTTTTTTCATTTCTCT
AATTCCGTGTTTAGATTGTACCTTACAGATGGTATTGGGTATTTCAAAAAAGTAAAGGA
3790 3800 3810 3820 3830 3840

CTATCTCTAATACACACTGTTCTTTCCAGACTTTCAACACGCTGCTATTTTTCTATTTTAT
GATAGAGATTATGTGTGACAAAGAAAGGTCTGAAAGTTGTGCGACGATAAAAGATAAAATA
3850 3860 3870 3880 3890 3900

TCAAGTCCATATTATAAGCGTCCCTTGTTAGACACTTCATAATGTTTGCATTCTGGAATCA
AGTTCAGGTATAAATATTCGCAGGAACAATCTGTGAAGTATTACAAACGTAAGACCTTAGT
3910 3920 3930 3940 3950 3960

REPLACEMENT SHEET

Figure 13 continued

T C A T G T T A G A T A C T A T T A A T T T A G C T A C T T C T A T G T T G T C A T C A A A A G A G T T G C T A T C T G
A G T A C A A T C T A T G A T A A T T A A A T C G A T G A A G A T A C A A C A G T A G T T T T C T C A A C G A T A G A C
3970 3980 3990 4000 4010 4020

T A A T T A C A C T A A G A G G T G T A T C A C C T G A T A A A G A A G T A A T A G A G A C A T C T G C T C T G A A T T
A T T A A T G T G A T T C T C C A C A T A G T G G A C T A T T T C T T C A T T A T C T C T G T A G A C G A G A C T T A A
4030 4040 4050 4060 4070 4080
T A A G C A A T A C C T C A A T A A C T T C T T T T G A A G A T G A C T T T G C A G C T A A A A A T A A T G G A G T T C
A T T C G T T A T G G A G T T A T T G A A G A A A C T T C T A C T G A A A C G T C G A T T T T T A T T A C C T C A A G
4090 4100 4110 4120 4130 4140

T C T C T A A A A C A T C C C T T G A G T T T A T A T T A G C C C C G T A A C T A A T G A G T A G T T C T G T T A T A T
A G A G A T T T T G T A G G G A A C T C A A A T A T A A T C G G G G C A T T G A T T A C T C A T C A A G A C A A T A T A
4150 4160 4170 4180 4190 4200

C T T T G G A A T C T A T T G A T A T A T T A T T A A T T A C A A T T G T C A T G C T G A C A T A T A T A G A C A T C A
G A A A C C T T A G A T A A C T A T A T A A T A A T T A A T G T T A A C A G T A C G A C T G T A T A T A T C T G T A G T
4210 4220 4230 4240 4250 4260

T A A T A T G A T G A A A A A T A T G A A A A T A T A A G T G C A C G T T T A C T G T T A C T A T G A T T G T G A T A T
A T T A T A C T A C T T T T T A T A C T T T T A T A T T C A C G T G C A A A T G A C A A T G A T A C T A A C A C T A T A
4270 4280 4290 4300 4310 4320

C G A T A T G A G T T C T T T A A T A A A A G T A C T G A A A T A G A T A T A A T G C A G A T A T G A T T G A T A T T T
G C T A T A C T C A A G A A A T T A T T T T C A T G A C T T T A T C T A T A T T A C G T C T A T A C T A A C T A T A A A
4330 4340 4350 4360 4370 4380

T A A A A A G T T G A A A A A A A T A T G C C C T G T T T A C A A A T A C T A T T T G G A A A T A T T C T G T A A T A
A T T T T T C A A C T T T T T T T A T A C G G G A C A A A T G T T T A T G A T A A A C C T T T A T A A G A C A T T A T
4390 4400 4410 4420 4430 4440

A A G T A A T A G T G A T A T G T C A G T C A C G A T G G A T T T G C C A A T T G A T C A T A T G A G T A T A G A T A A
T T C A T T A T C A C T A T A C A G T C A G T G C T A C C T A A A C G G T T A A C T A G T A T A C T C A T A T C T A T T
4450 4460 4470 4480 4490 4500

C A T A A A C G A G T A T A A T A A A A A T G G A T A T A C T A G A C T C T A T A T A G A G G T A G C C A T G A A A A A
G T A T T T G C T C A T A T T A T T T T T A C C T A T A T G A T C T G A G A T A T A T C T C C A T C G G T A C T T T T T
4510 4520 4530 4540 4550 4560

REPLACEMENT SHEET

Figure 13 continued

ACGTAAAAACGTAGATAGACTTTTATATCTCGGAGCTGATCCGAATCTGGCTAGTGTAGA
TGCATTTTTTGCATCTATCTGAAAAATATAGAGCCTCGACTAGGCTTAGACCGATCACATCT
4570 4580 4590 4600 4610 4620

TTCGTATTGTCTCTTCATATTGCTGTTAGGAATGGTAGTTTAAAGATAATAAGATCATT
AAGCATAACAGGAGAAGTATAACGACAATCCTTACCATCAAATTTCTATTATTCTAGTAA
4630 4640 4650 4660 4670 4680

GTTGAAATATGGTGCTAATATAAATCAAGAATGTCATGAAGGAGATACTGCTTTGATGAT
CAACTTTTATACCACGATTATATTTAGTTCTTACAGTACTTCTCTATGACGAAACTACTA
4690 4700 4710 4720 4730 4740

GGCTATATCATTAGGTAATTATACAGCATGTAAACACTTCTAGATAAACACGCCGATCC
CCGATATAGTAATCCATTAAATATGTCGTACATTTTGTGAAGATCTATTGTTGCGGCTAGG
4750 4760 4770 4780 4790 4800

TAAATTATGTTAACTATTACGGTATAGTTCCGCTTATTAGAGCAATTATATGTGAAAAGCC
ATTAATACAATTGATAATGCCATATCAAGGCGAATAATCTCGTTAATATACACTTTTTCGG
4810 4820 4830 4840 4850 4860

TGACATAGTTAGACTGCTATTAGATAGAGGAGCTAATTGCAACCACCTTAATTACAAAAAA
ACTGTATCAATCTGACGATAATCTATCTCCTCGATTAAAGTTGGTGAATTAATGTTTTTT
4870 4880 4890 4900 4910 4920

CGGTAGAACCTATACTGCTTTAGAGAGTCTTAGGAATTGCTTTTTTAAAGACAATTCTTC
GCCATCTTGGATATGACGAAATCTCTCAGAATCCTTAACGAAAAAATTTCTGTTAAGAAG
4930 4940 4950 4960 4970 4980

ATCATTTGTCGATACTAATAT
TAGTAACAGCTATGATTATA
4990 5000